

DESCRIPTION

PROBE SET AND METHOD FOR IDENTIFYING HLA ALLELE

TECHNICAL FIELD

5 The present invention relates to a probe set and a method for identifying an allele of human HLA.

BACKGROUND ART

Human leukocyte antigen (HLA) is known to
10 include multiple HLA types, such as HLA-A, HLA-B, HLA-C, HLA-DP, HLA-DQ, HLA-DR, and HLA-MICA. An HLA allele is designated with a four or more digit number by the WHO HLA Nomenclature Committee. The principle of the nomenclature is that the first two digits
15 correspond to the serotypes; the third and fourth digits distinguish the alleles of different amino acid sequences (subtypes); and the fifth digit distinguishes the alleles of different base sequences but encoding the same amino acid sequence. Typing of
20 these alleles has been conventionally conducted at the serological level. Although this serological method does not require special sample processing, and enables easy typing using antigen-antibody reaction, the serotypes are the roughest
25 classification corresponding to the first two digits of the numbers according to the nomenclature described above.

Many of other commercially available kits of the type associated with genomic extraction do not have enough accuracy to identify each allele individually. It is the current state that such a
5 kit distinguishes multiple alleles as a group. Moreover, even a kit based on the SBT (Sequencing Based Typing) method, which enables the most detailed polymorphic analysis, often fails to solve the problem of ambiguity by one analysis since most
10 samples are heterozygotes requiring reexamination. Such problematic alleles are listed collectively in <http://www.ihwg.org/protocols/sbt/ambiguities2.pdf> by the International Histocompatibility Working Group (IHWG).

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DISCLOSURE OF INVENTION

On the other hand, with the development of advanced medical treatment in recent years, detailed HLA typing is required in organ transplantation, etc.
20 In addition, associations of HLA with diabetes, cancer, and other multifactorial diseases have been suggested. With such a background, a test method is desired that can identify each allele individually. Upon such demands it is an object of the present
25 invention to provide a probe set that is useful for identifying each allele of HLA individually, and a method for identification of an HLA allele by the use

thereof.

A probe set for identifying an allele of HLA according to the present invention is a probe set comprising multiple probes that can be used for
5 identifying HLA allele contained in a specimen, characterized in that each of the multiple probes comprises a partial sequence containing a base represented by a capital letter in a sequence of each allele in an allele list in the description.

10 An embodiment of the present invention is a probe set comprising multiple probes that can be used for identification of an HLA-A allele in a specimen, characterized in that each of the multiple probes comprises a partial sequence containing a base
15 represented by a capital letter in a sequence of each allele in an allele list in the description.

Another embodiment of the present invention is a method for identification of an HLA-A allele contained in a specimen using a probe set,
20 characterized in that the probe set is the probe set described above.

Another embodiment of the present invention is a probe set comprising multiple probes that can be used for identification of an HLA-B allele in a
25 specimen, characterized in that each of the multiple probes comprises a partial sequence containing a base represented by a capital letter in a sequence of each

allele in an allele list in the description.

Another embodiment of the present invention is a method for identification of an HLA-B allele contained in a specimen using a probe set,
5 characterized in that the probe set is the probe set described above.

Another embodiment of the present invention is a probe set comprising multiple probes that can be used for identification of an HLA-C allele in a
10 specimen, characterized in that each of the multiple probes comprises a partial sequence containing a base represented by a capital letter in a sequence of each allele in an allele list in the description.

Another embodiment of the present invention is
15 a method for identification of an HLA-C allele contained in a specimen using a probe set, characterized in that the probe set is the probe set described above.

Another embodiment of the present invention is
20 a probe set comprising multiple probes that can be used for identification of an HLA-DP allele in a specimen, characterized in that each of the multiple probes comprises a partial sequence including a base represented by a capital letter in the sequence of
25 each allele in the allele list in the description.

Another embodiment of the present invention is a method for identification of an HLA-DP allele

contained in a specimen using a probe set,
characterized in that the probe set is the probe set
described above. Another embodiment according to the
present invention is a probe set for identification
5 of an HLA-DQ allele that is a probe set comprising
multiple probes that can be used for identification
of an HLA-DQ allele in a specimen, characterized in
that each of the multiple probes comprises a partial
sequence containing a base represented by a capital
10 letter in a sequence of each allele in an allele list
in the description.

Another embodiment of the present invention is
a probe set comprising multiple probes that can be
used for identification of an HLA-DQ allele in a
15 specimen, characterized in that each of the multiple
probes comprises a partial sequence containing a base
represented by a capital letter in a sequence of each
allele in an allele list in the description.

Another embodiment of the present invention is
20 a method for identification of an HLA-DQ allele
contained in a specimen using a probe set,
characterized in that the probe set is the probe set
described above.

Another embodiment of the present invention is
25 a probe set comprising multiple probes that can be
used for identification of an HLA-DR allele in a
specimen, characterized in that each of the multiple

probes comprises a partial sequence containing a base represented by a capital letter in a sequence of each allele in an allele list in the description.

Another embodiment of the present invention is
5 a method for identification of an HLA-DR allele contained in a specimen using a probe set, characterized in that the probe set is the probe set described above.

Another embodiment of the present invention is
10 a probe set comprising multiple probes that can be used for identification of an HLA-MICA allele in a specimen, characterized in that each of the multiple probes comprises a partial sequence containing a base represented by a capital letter in a sequence of each
15 allele in an allele list in the description.

Another embodiment of the present invention is a method for identification of an HLA-MICA allele contained in a specimen using a probe set, characterized in that the probe set is the probe set
20 described above.

The probe set according to the present invention, and identification of an allele of each HLA type by the use thereof can contribute to diathesis diagnoses and tailor-made medicines, which
25 are required in organ transplantation, cancer, diabetes, and other multifactorial diseases.

Other features and advantages of the present

invention will be apparent from the following description.

BEST MODE FOR CARRYING OUT THE INVENTION

5 Preferred embodiments of the present invention will now be described in detail. Each probe that constitutes the probe set of the present invention has a partial sequence including a base represented by a capital letter in each allele sequence in the
10 allele lists described later. Preferably, segments consisting of 10 to 30 bases including a base represented by a capital letter are selected from each allele sequence, and the probe set is composed of probes having the obtained partial base sequences
15 respectively. As specific examples, the following compositions can be employed:

1) A probe set for HLA-A allele identification consisting of respective probes listed in one of the probe list A1 shown in Tables 1-1 to 1-7 and the
20 probe list A2 shown in Tables 2-1 to 2-6 shown later;

2) A probe set for HLA-B allele identification consisting of probes listed in one of the probe list B1 shown in Tables 5-1 to 5-9 and the probe list B2 shown in Tables 6-1 to 6-8 shown later;

25 3) A probe set for HLA-C allele identification consisting of probes listed in one of the probe list C1 shown in Tables 9 and the probe list C2 shown in

Table 10 shown later;

4) A probe set for HLA-DP allele identification consisting of probes listed in one of the probe lists DP1-DP4 shown in Tables 13-1 to 16-5 respectively as
5 shown later;

5) A probe set for HLA-DQ allele identification consisting of probes listed in one of the probe lists DQ1 to DQ 4 shown in Tables 17A, 17B-1, 17B-2, 18A, 18B-1 and 18B-2 respectively as shown later;

10 6) A probe set for HLA-DR allele identification consisting of probes listed in one of the probe lists DR1 and DR2 shown in Tables 21-1 to 21-8 and Tables 22-1 to 22-7 respectively, as shown later; and

7) A probe set for HLA-MICA allele
15 identification consisting of probes listed in one of the probe lists MICA1 and MICA2 shown in Tables 25-1, 25-2 and Tables 26-1 to 26-2 respectively, as shown later.

For example, the No.0 probe in the probe list
20 A1 has a 16-base sequence of "gccccgcttcatcgcC", which is a segment containing the first capital lettered base C in A*010101, and the No.0 probe in the probe list 2 has an 18-base sequence of "cttcatcgcCgtgggcta", which is a segment also
25 containing the first capital lettered base C in the same allele.

In the allele list, each allele is assigned

with a unique number such as "A*xxxx" in accordance with "allele nomenclature" by Japanese Society for Histocompatibility and Immunogenetics, HLA Standardization Committee.

5 To identify an allele using a probe set according to the present invention, two methods are possible: one is detection by hybridization; and the other is direct detection by PCR without hybridization. In either method, each probe is an
10 oligonucleotide of preferably more than 10 and less than 30 nucleotides in length and designed to include the base represented by a capital letter, i.e., a base specific for the allele to be identified.

 Moreover, the probe arrays provided in the
15 present invention present groups of varied bases for identification of each allele individually by positions chosen for the probes. As a method for detection of such a varied base, the detection method by hybridization, and the method of direct detection
20 by PCR without hybridization can also be preferably used. Also in these cases, the probes are designed as oligonucleotides of preferably more than 10 and less than 30 nucleotides in length each containing a base represented by a capital letter.

25 When a variation is detected by hybridization, probes are preferably designed to have a variant base represented by a capital letter near the center of

the probes, which makes T_m difference between full-matched and mismatched pairs larger, enabling easier separation of them by adjusting the reaction temperature of hybridization.

5 On the other hand, when the variation is directly detected by PCR, the variant base is rather placed near the 3' end so that enzymatic recognition and elongation of annealed double strands will not occur. Also, some variation methods are possible,
10 such as a method placing a variant base at the second from the 3' end an artificial variant base at the third from the 3' end as with Allele Specific Primer (Toyobo Co., Ltd.); a method circularizing probes by ligation with a mismatch placed near the 3' end
15 (Amersham Biosciences Co., Ltd.); TaqMan-MGB (ABI Co.); and 3'-end mismatch using LNA (Proligo Japan Co., Ltd.).

For example, a segment including the fourth capital letter of A*2302 is "ggagcagTggagagC", and
20 the corresponding segment of A*2303 of the same serotype is "ggagcagtTgagagc", differing at the ninth base. By using a probe with a sequence of one of these segments, one can be distinguished from the other by mismatching.

[EXAMPLES]

The present invention will be described further by way of examples in the following. The SEQ ID NOS of the sequences in Examples are in the following relation:

Examples 1 and 2: Sequence Listing A

Examples 3 and 4: Sequence Listing B

Examples 5 and 6: Sequence Listing C

Examples 7 and 8: Sequence Listing DP

10 Examples 9 and 10: Sequence Listing DQ

Examples 11 and 12: Sequence Listing DR

Examples 13 and 14: Sequence Listing MICA.

(Example 1)

15 Probes for identification of HLA-A allele

Extraction of DNA from 1 ml of human blood was performed using GFX Genomic Blood DNA Purification Kit from Amersham Biosciences. The protocol is as follows:

20 Blood 1 ml →

Add RBC Lysis Solution [hemolysate] →

Mix gently at room temperature for 5 minutes →

Centrifuge at 12,000-16,000 × g for 20 seconds →

Discard the supernatant leaving 20-50 µl →

25 Resuspend the precipitation →

Add Extraction Solution and vortex vigorously →

Stand at room temperature for 5 minutes [extraction

of DNA] →

Set a GFX Column in a Collection Tube →

Heat the elution buffer to 70°C →

Add the sample →

5 Centrifuge at 5,000 × g for 1 minute (binding of DNA)

→

Add Extraction Solution (washing) →

Centrifuge at 5,000 × g for 1 minute →

Add Washing Solution (washing) →

10 Centrifuge at 12,000 × g for 3 minutes →

Set a GFX Column in a centrifugal tube →

Elate with pure water →

Stand at room temperature for 1 minute →

Centrifuge at 5,000-8,000 × g for 1 minute →

15 Concentrate to 230 µl solution (1).

Next, quantitative PCR was carried out using
QuantiTect SYBR Green PCR Kit from QIAGEN and
GeneAmp5700 from ABI. The reaction composition and
20 the protocol are shown below.

1) Reaction composition/well (96 well microplate)

QuantiTect SYBR Green 2 × premix: 10 µl

Solution (1): 1 µl

Solution of one of the probes in the probe list

25 A1(10 pmol/µl): 1 µl

Mixed primers (10 pmol/µl)*: 3 µl

Ultra pure water: 5 µl

(Total: 20 μ l)

*consisting of 1 μ l each of the solutions respectively containing probes of the following sequences at 10 pmol/ μ l:

5 CCCATCTCAGGGTGAGGGGCT (SEQ ID NO: 632)

GCGCTGCAGCGTCTCCTTCC (SEQ ID NO: 633)

GCCCAGGTCTGGGTCAGGGCCAG (SEQ ID NO: 634)

2) PCR program

94°C: 180 sec followed by 30 cycles of [94°C: 10
10 sec \rightarrow 66°C: 10 sec \rightarrow 72°C: 20 sec.].

Referring to Amp Plot and Dissociation curves on a display of 5700 software, and to the allele-probe correspondence list A1 (Tables 3-1 to 3-9), it was identified as A*2402101.

15

(Example 2)

Extraction of DNA from 1 ml of human blood was performed in the same manner as in Example 1. PCR of human HLA-A was then performed using ABI 9700 PCR
20 Instrument and Ex Taq from Takara Bio Inc. The reaction composition and the protocol are as follows:

1) Reaction composition/tube

Ex Taq 2 \times premix: 20 μ l

Solution (1): 3 μ l

25 Cy-3 dUTP (1 mM): 2 μ l

Mix primer (10 pmol/ μ l)*: 3 μ l

Ultra pure water: 12 μ l

(Total: 40 μ l)

*consisting 1 μ l each of the solutions
respectively containing probes of the following
sequences at 10 pmol/ μ l:

- 5 ATGGCTCCCCGAACCCTC (SEQ ID NO: 635)
 ATGGCGCCCCGAACCCTC (SEQ ID NO: 636)
 CATCTCAGGGTGAGGGGCT (SEQ ID NO: 637)

2) PCR program

94°C: 180 sec followed by 30 cycles of [94°C: 10
10 sec → 66°C: 10 sec → 72°C: 20 sec]

After the completion of the reaction, unreacted
dNTPs, etc., were removed using a purification column
(QIAGEN QIAquick PCR Purification Kit) to obtain a
sample.

- 15 At the same time, a DNA microarray was prepared
to identify the allele in the specimen described
above. The method for the preparation was in
accordance with examples in Japanese Patent
Application Laid-Open No. H11-187900. SH group was
20 used as the functional group for immobilization. A
glass substrate was treated by a silane-coupling
agent to bind the SH group of the probes via a
divalent reagent EMCS (N-(6-
maleimidocaproyloxy)succinimide). Each probe in the
25 probe list A2 was used for each dot.

The DNA microarray was blocked in advance with
PBS supplemented with 1 wt% of BSA (bovine serum

albumin) for two hours. The sample was adjusted to have a salt concentration equal to that of the PBS, and to contain 0.1 wt% of SDS (sodium dodecyl sulfate) and 25% of formamide.

5 Then, hybridization was performed using the above sample (PCR product) and the prepared DNA microarray. 50 μ l of the sample was reacted with the blocked DNA microarray at 60 °C for 2 hours. Unreacted substances were washed off by washing three
10 times with 2 x SSC solution (NaCl 300 mM, Sodium Citrate (trisodium citrate dihydrate, $C_6H_5Na_3 \cdot 2H_2O$) 30 mM, pH 7.0), followed by washing twice with 0.1 x SSC solution. The DNA microarray was air-dried and the fluorometry measurement was conducted using
15 GenePix4000B made by Axon. Referring to the allele-probe list A2 (Tables 4-1 to 4-9), the sample was identified as A*2402101.

A*010101 :

atggccgctcatggcgccccgaacccctcctcctgctactcgcggggccctggccctgacccagaccctggcgggct
20 cccactccatgaggtattcttcacatccgtgtccggcccgccgcccggagccccgcctcatcgcCgtgggcta
cgtggacgacacgcagttcgtgcggttcgacagcgacccgcgagccagaagatggagccgcccggcgccgtggata
gagcaggaggggcccggaglatitgggaccaggagacacggaatAtgaaggccactcacagactgaccgagcgaacc
tggggacccctgcgcggctactacaaccagagcgaggacgggttcacaccatccagataatgtatggctgcgacgt
ggggccggacggcgcttctccgcccgtaccggcaggacgcctacgacggcaaggattacatgccctgaacgag
25 gacctgcgtctcttggaccgcccggacatggcagctcagatcaccaagcgcaagtgggaggcgggtccatgcggcgg
agcagcggagagTctaccitggagggcCGgtgcgtggacgggtccgcagataacctggagaacgggaaggagacgct
gcagcgcacggaccccccaagacacatatgaccaccaccccatctctgacatgaggccacccctgaggtgcctgg

gccccGgccttctacccTgcggagatcacactgacctggcagcgggatggggaggaccagaccaggacacggagc
tcgtggagaccaggccTgcaggggatggaacctTccagaagtgggcggctTgTggTggTgccttctTggaGaggagca
gagatacacctTgcatTgtcagcatgagggTctgccaagccccTcacctTgagatgggag (SEQ ID
NO:1) ;

5 A*010102 :

gcTcccacTccatgagglatttctTcacatccgtTgTcccggccccggcgcggggagccccgcTtcaTcgccgtggg
ctacgtggagacacgcagTtcgtTcggtTcgacagcgacgccgcgagccagaagatggagccgcgggcggcgtgg
atagagcaggagggggccggagTatTgggaccaggagacacggaataTgaaggccacTcacagacTgaccgagcga
acctggggacccTgcgcggctactacaaccagagcgaggacggTtTcacacacTccagataatgtatggctTcga
10 cgtggggccggacgggcgtTccTccgcgggtaccggcaggacgcctacgacggcaaggatTacatcgccTgaac
gaggacctgcgcTctTggaccgcggcgacatggcagctcagatTaccaagcgcaagtgggaggcggTccatgcgg
cggagcagcggagagTctacctggagggccggTgcgtggacgggcTccgcagatacctggagaacgggaaggagac
gcTgcagcgacgg (SEQ ID NO: 2) ;

A*0102 :

15 atggccgtcatggcgcccgaacccTccTctgtTactTcTgggggccTggccTgaccagacctgggcgggcT
cccacTccatgaggtatttctTcacatccgtTgTcccggccccggcagTggAgagccccgcTtcaTcgagTggcTca
cgTggacgacacgcagTtcgtTcggtTcgacagcgacgccgcgagccagaagatggagccgcgggcggcgtggata
gagcaggagggggccggagTatTgggaccaggagacacggaataTgaaggccacTcacagacTgaccgagcgaacc
TggggacccTgcgcggctactacaaccagagcgaggacggTtTcacacacTccagataatgtatggctTgcgacgt
20 ggggccggacgggcgtTccTccgcgggtaccggcaggacgcctacgacggcaaggatTacatcgccTgaacgag
gacctgcgcTctTggaccgcggcgacatggcagctcagatTaccaagcgcaagtgggaggcggTccatgcggcgg
agcagcggagagTctacctggagggccggTgcgtggacgggcTccgcagatacctggagaacgggaaggagacgt
gcagcgacggaccccccaagacacataTgaccaccacccacTctTgacatgaggccacccTgaggtgcTgg
gcccTgggcTtctacccTgcggagatcacactgacctggcagcgggatggggaggaccagaccaggacacggagc
25 tcgtggagaccaggccTgcaggggatggaacctTccagaagtgggcggctTgTggTggTgccttctTggagaggagca
gagatacacctTgcatTgtcagcatgagggTctgccaagccccTcacctTgagatgggag (SEQ ID NO: 3)

A*0103 :

gctcccacitccatgaggatattcttcacatccgtgtcccggccccggccgaggagccccgcttcatcgccgtggg
ctacgtggacgacacgcagttcgtgcggttcgacagcgacgccgcgagccagaagaatggagccgcgggcgccgtgg
atagagcaggaggggcccggagtattgggaccaggagacacggaalatgaaggcccactcacagactgaccgagcga
acctggggacccitgcgcggctactacaaccagagcgaggacgggttctcacaccatccagatgaigtatggctgcga
5 cgtggggccggacgggcgttccctccgcggtaccggcaggacgcctacgacggcaaggattacatcgccctgaac
gaggacctgcgctcttggaccgcgcgacatggcagctcagatcaccaagcgcaagtgaggaggcggttccatgcgg
cggagcagcggagagcttaccitggagggccggitgcgtggacgggtccgcagatacctggagaacgggaaggagac
gctgcagcgcacgg (SEQ ID NO: 4) ;

A*0106 :

10 gctcccacitccatgaggatattcttcacatccgtgtcccggccccggccgaggagccccgcttcatcgccgtggg
ctacgtggacgacacgcagttcgtgcggttcgacagcgacgccgcgagccagaagaatggagccgcgggcgccgtgg
atagagcaggaggggcccggagtattgggaccaggagacacggaalatgaaggcccactcacagactgaccgagcga
acctggggacccitgcgcggctactacaaccagagcgaggacgggttctcacaccatccagataaigtatggctgcga
cgtggggccggacgggcgttccctccgcggtaccggcaggacgcctacgacggcaaggattacatcgccctgaac
15 gaggacctgcgctcttggaccgcgcgacatggcagctcagatcaccaagcgcaagtgaggaggcggttccatgcgg
cggagcagTTgagagcttaccitggagggccggitgcgtggacgggtccgcagatacctggagaacgggaaggagac
gctgcagcgcacgg (SEQ ID NO:5) ;

A*0107 :

gctcccacitccatgaggatattcttcacatccgtgtcccggccccggccgaggagccccgcttcatcgccgtggg
20 ctacgtggacgacacgcagttcgtgcggttcgacagcgacgccgcgagccagaagaatggagccgcgggcgccgtgg
atagagcaggagaggccTgagtattgggaccaggagacacggaaltgaaggcccactcacagactgaccgagAga
acctggggacccitgcgcggctactacaaccagagcgaggCgggttctcacaccatccagataaigtatggctgcga
cgtggggccggacgggcgttccctccgcggtaccggcaggacgcctacgacggcaaggattacatcgccctgaac
gaggacctgcgctcttggaccgcgcgacatggcagctcagatcaccaagcgcaagtgaggaggcggttccatgcgg
25 cggagcagcggagagcttaccitggagggccggitgcgtggacgggtccgcagatacctggagaacgggaaggagac
gctgcagcgcacgg (SEQ ID NO: 6) ;

A*0108 :

gc|cccactcca|gaggtatt|cttcacatccgtg|tcccggcccgccgcggggagccccgct|catcgccgtggg
ctacgtggacgacacgcagttcgtgcggttcgacagcgacgccgcgagccagaagatggagccgcgggcgccgtgg
atagagcaggagggggccggaglat|gggaccaggagacacggaata|gaaggccac|cacagac|gaccgagcga
acctggggaccc|gcgcggctactacaaccagagcgaggacgg|tctcacaccatccagataatgtatggctgcga
5 cgtggggccggacgggcgtt|cctccgcgggtaccggcaggacgct|acgacggcaaggattacatcgccctgaac
gaggacctgcgctct|ggaccgcggcggacat|ggcagctcagatcaccaagcgcaag|gggaggcgggtccatgcgg
cggagcagcggagagct|acctggagggcTgg|tgcgtggacgggtccgcagat|acctggagaacgggaaggagac
gctgcagcgacgg (SEQ ID NO: 7) ;

A*0109 :

10 atggccgtcat|ggcgccccgaaccctcc|ctgtctac|ctcggggccct|ggccctgaccagacct|gggcgggct
cccactcca|gaggtatt|cttcacatccgtg|tcccggcccgccgcggggagccccgct|catcgccgtgggcta
cgtggacgacacgcagttAg|tgcggttcgacagcgacgccgcgagccagaagatggagccgcgggcgccgtggata
gagcaggagggggccggaglat|gggaccaggagacacggaata|gaaggccac|cacagac|gaccgagcgaacc
tggggaccc|gcgcggctactacaaccagagcgaggacgg|tctcacaccatccagataatgtatggctgcgacgt
15 ggggcccggacgggcgtt|cctccgcgggtaccggcaggacgct|acgacggcaaggattacatcgccctgaacgag
gacctgcgctct|ggaccgcggcggacat|ggcagctcagatcaccaagcgcaag|gggaggcgggtccat|cggcgcg
agcagcggagagct|acctggagggccgg|tgcgtggacgggtccgcagat|acctggagaacgggaaggagacgt
gcagcgcacggaccccccaagacacat|gaccaccaccccatct|tgacat|gaggccacct|gagg|tgc|tgg
gccc|tgggtt|ct|acct|gcggagat|cacac|gacct|ggcagcggga|tggggaggaccagaccaggacacggagc
20 tct|ggagaccaggcc|gcagggga|ggaacct|ccagaag|tggcggt|t|gg|tgg|tgc|t|t|ggagaggagca
gagatacacct|gcat|gtgcagcat|gagggt|t|gccaagcccc|cacct|gaga|tgggag (SEQ ID NO:
8) ;

A*020101 :

atggccgtcat|ggcgccccgaaccctc|gtctgtac|ctcggggcTc|tggccctgaccagacct|gggcgggct
25 ct|cac|tcca|t|gaggtatt|cttcacatccgtg|tcccggcccgccgcggggagccccgct|catcgag|tgggcta
cgtggacgacacgcagttcgtgcggttcgacagcgacgccgcgagccagaggatggagccgcgggcgccgtggata
gagcaggaggg|tccggaglat|gggacggggagacacggaaAg|tgaaggccac|cacagac|Caccgag|tggacc

aaacgcataatgactcaccacgcgtgtcttgaccaatgaagccacccigaggtagcggggcccgagccttaccctgc
ggagatcacacigaccitggcagcgggatggggaggaccagaccaggacacggagctcgtggagaccaggccatgca
ggggatggaaaccttccagaagtggcgggcgtgtgggtgccttcgtggacaggagcagagatacaccitgccatgtgc
agcatgagggtttgcccagccctcaccctgagatggg (SEQ ID NO: 11) ;

5 A*020104 :

gctctcactccatgaggatattcttcacatccgtgtcccgcccgccggggagccccgcttcatcgcagtggg
ctacgtggacgacacgcagttcgtgcgttcgacagcgacgccgcgagccagaggatggagccgcggcgccgtgg
atagagcaggagggtccggagtattgggacggggagacacggaaagtgaaggccactcacagactcaccgagtgg
acctggggacccitgcgcggctactacaaccagagtgaggccggttctcacaccgtccagaggatgtatggctgcga
10 cgtgggggtcggactggcgcttccitccgcggttaccaccagttacgcttacgacggcaaggattacatcgccctgaaa
gaggacctgcgctcttggaccgcAgcggacatggcagctcagaccaccaagcacaagtgggaggcgcccatgttg
cggagcagttgagagcctacctggagggcacgtgcgtggagtggctccgcagataccitggagaacgggaaggagac
gctgcagcgcacgg (SEQ ID NO: 12)

A*020105 :

15 gctctcactccatgaggatattcttcacatccgtgtcccgcccgccggggagccccgcttcatcgcagtggg
ctacgtggacgacacgcagttcgtgcgttcgacagcgacgccgcgagccagaggatggagccgcggcgccgtgg
atagagcaggagggtccggagtattgggacggggagacacggaaagtgaaggccactcacagactcaccgagtgg
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A*0203 :

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A*0208 ;

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A*0210 :

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A*0214 :

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5 A*0216 :

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A*0218 :

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5 A*0219 :

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A*022001 :

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5 A*0221 :

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A*0222 :

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15 A*0225 :
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10 A*0230 :

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gctgcagcgacgg (SEQ ID NO:50) ;

15 A*0236 :

gctctcactccatgaggtaattctctcacatccgtgtcccgccccggcggggagccccgcttcatcgcatggg
ctacgtggagacacgcagttcgtgcggttcgacagcgacgccgagccagaggatggagccgccccgctgg
atagagcaggagggtccggagtaattgggacGggagacacggaaAgigaaggcccatcacagactCaccgagttg
acctggggaccttgcgcggctactacaaccagagcgaggccggtctctcacaccGtccagaGgaigtatggctgcga
20 cgtggggctcgacTggcgcttctccgcggttaccacagTaccgctacgacggcaaggattacatcgccctgaaA
gaggacctgcgctcttggaccgcgcgacatggcagctcagaCcaccaagcacaagtgggaggcgccccatgTgg
cggagcagTgagagccctacctggagggaCgtgcgtggacgggtccgcagataacctggagaacgggaaggagac
gctgcagcgacgg (SEQ ID NO:51) ;

A*0237 :

25 gctctcactccatgaggtaattctctcacatccgtgtcccgccccggcggggagccccgcttcatcgcatggg
ctacgtggagacacgcagttcgtgcggttcgacagcgacgccgagccagaggatggagccgccccgctgg
atagagcaggagggtccggagtaattgggacggggagacacggaaagtgaaggcccatcacagactcaccgagttg

accTggggaccctgcgcggctacIacaacCagagcgaggccggTtctcacaccGtccagaggatgtatggctgcga
cgTggggTcggactggcgcttccTccgCGggtaccaccagTaccctacgacggcaaggattacatcgccctgaaa
gaggaccTgcgcTctTggaccgCGcggaCaTggcagctcagaccaccaagcAcaagTgggagggcgcccatgTgg
cggagcagcAgagagcctaccTggagggc aCgtgcTggacgggctccgcagataccTggagaacgggaaggagac
5 gctgcagcgcacgg (SEQ ID NO:52) ;

A*0238 :

gctctcactccaTgaggTatttctIcacaTccgtgtcccgcccgccgCGgggagccccgctIcaTcgcaTggg
ctacTggacgacacgcagTtctgtcggtTcgacagcgacgccgCGagccagaggatggagccgCGggcgccgtgg
atagagcaggagggTccggagTatTgggaCGgggagacacggaaagTgaaggccctcacagactcaccgagTgg
10 accTggggaccctgcgcggctacIacaacCagagcgaggccggTtctcacaccgtccagaggatgtatggctgcga
cgTggggTcggactggcgcttccTccgCGggtaccaccagTaccctacgacggcaaggattacatcgccctgaaa
gaggaccTgcgcTctTggaccgCGcggaCaTggcagctcagaccaccaagcAcaagTgggagAcggcccatgagg
cggagcagcAgagagcctaccTggagggcCGgtgcTggagTggctccgcagataccTggagaacgggaaggagac
gctgcagcgcacgg (SEQ ID NO:53) ;

15 A*0239 :

gctctcactccaTgaggTatttctIcacaTccgtgtcccgcccgccgCGgggagccccgctIcaTcgcaTggg
ctacTggacgacacgcagTtctgtcggtTcgacagcgacgccgCGagccagaggatggagccgCGggcgccgtgg
atagagcaggagggTccggagTatTgggaCGgggagacacggaaagTgaaggccctcacagactcaccgagTgg
accTggggaccctgcgcggctacIacaacCagagcgaggccggTtctcacaccgtccagaggatgtTggctgcga
20 cgTggggTcggacggcgcttccTccgCGggtaccaccagTaccctacgacggcaaggattacatcgccctgaaa
gaggaccTgcgcTctTggaccgCGcggaCaTggcGgtcagatcaccaagcAcaagTgggagggcgcccatgTgg
cggagcagTgagagCctaccTggagggc aCgtgcTgggaGTggctccgcagataccTggagaacgggaaggagac
gctgcagcgcacgg (SEQ ID NO:54) ;

A*0240 :

25 gctctcactccaTgaggTatttctIcacaTccgtgtcccgcccgccgCGgggagccccgctIcaTcgcaTggg
ctacTggacgacacgcagTtctgtcggtTcgacagcgacgccgCGagccagaggatggagccgCGggcgccgtgg
atagagcaggagggTccggagTatTgggaCGgggagacacggaaagTgaaggccctcacagactcaccgagTgg

accctggggacccctgcgcggctactacaaccagagcgaggccgggtctctacaccgtccagaggatglatggctgcga
cgtggggctcggactggcgcttccctcgcgggtaccaccagtagcctacgacggcaaggattacatcgccctgaaa
gaggacctgcgctcttggaccgcgccggacatggcagctcagaccaccaagcAcaagtgggaggcgggccGtGTgg
cggagcagttgagagcctaccctggagggcaCgtgcgtggagTggctccgcagataccctggagaacgggaaggagac
5 gctgcagcgcacgg(SEQ ID NO: 55) ;

A*0241 :

gctctcactccatgaggtatttctacacCtccgtgtcccgcccgccgaggagccccgcttcatcgcAgTggg
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atagagcaggagggctccggagtattgggacgGggagacacggaaAgTgaaggccctcacagactCaccgagttg
10 accctggggacccctgcgcggctactacaaccagagcgaggccgggtctctacaccGtccagaGgatglatggctgcga
cgtggggctcggactggcgcttccctcgcgggtaccagcagTaccgttacgacggcaaggattacatcgccctgaaa
gaggacctgcgctcttggaccgcgccggacatggcagctcagaCcaccaagcacaagtgggaggcgggccatGTgg
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gctgcagcgcacgg(SEQ ID NO: 56) ;

15 A*0242 :

gctctcactccatgaggtatttcttccatccgtgtcccgcccgccgaggagccccgcttcatcTcagtggg
ctacgtggacgacacgcagttcgtgcgggttcgacagcgacgccgagccagaggatggagccgcggcgccgtgg
atagagcaggagggctccggagtattgggacggggagacacggaaagtgaaggccctcacagactcaccgagttg
accctggggacccctgcgcggctactacaaccagagcgaggccgggtctctacaccgtccagaggatglatggctgcga
20 cgtggggctcggactggcgcttccctcgcgggtaccaccagtagcctacgacggcaaggattacatcgccctgaaa
gaggacctgcgctcttggaccgcgccggacatggcagctcagaccaccaagcacaagtgggaggcgggccatgtgg
cggagcagttgagagcctaccctggagggcacgtgcgtggagTggctccgcagataccctggagaacgggaaggagac
gctgcagcgcacgg(SEQ ID NO: 57) ;

A*0244 :

25 gctctcactccatgaggtatttctacacCtccgtgtcccgcccgccgaggagccccgcttcatcgcagtggg
ctacgtggacgacacgcagttcgtgcgggttcgacagcgacgccgagccagaggatggagccgcggcgccgtgg
atagagcaggagggctccggagtattgggacggggagacacggaaagtgaaggccctcacagactcaccgagttg

accitggggaccctgcgcggctactacaaccagagcgaggccgggttctcacaccGtccagaggaigtatggctgcga
cgtggggctcggactggcgcttccctccgcgggtaccaccagtagcctacgacggcaaggattacatcgccctgaaa
gaggacctgcgctcttggaccgcgccggacatggcagctcagatcaccaagcgaagtgaggaggcgcccaatgTgg
cggagcagcAgagagccctaccitggaggggcaCgtgcgtggagTggctccgcagataccitggagaacgggaaggagac
5 gctgcagcgcacgg (SEQ ID NO:58) ;

A*0245 :

gctctcacctccatgaggtaattcttcacatccgtgtcccgcccgccggggagccccgcttcatcgcAgtggg
ctacgtggacgacacgcagttcgtgcgggtcgacagcgacgccgcgagccagaggatggagccgcggcgccgtgg
atagagcaggagggtccggagtattgggaccaggagacacggaaAgtgaaggccctcacagactCaccgagtgg
10 accitggggaccctgcgcggctactacaaccagagcgaggccgggttctcacaccGtccagaGgatgtatggctgcga
cgtggggctcggacTggcgcttccctccgcgggtaccaCagTaccgtacgacggcaaggattacatcgccctgaaaA
gaggacctgcgctcttggaccgcgccggacatggcagctcagaCcaccaagcacaagtgaggaggcgcccaatgTgg
cggagcagITgagagccctaccitggaggggcaCgtgcgtggagTggctccgcagataccitggagaacgggaaggagac
gctgcagcgcacgg (SEQ ID NO:59) ;

15 A*0246 :

atggccgtcatggcgccccgaaccctcgtctgtactctcgggggcTctggccctgaccagacctgggcgggct
ctcacctccatgaggtaattcttcacatccgtgtcccgcccgcccgggggagccccgcttcatcgcagtgggcta
cgtggacgacacgcagttcgtgcgggtcgacagcgacgccgcgagccagaggatggagccgcggcgccgtggata
gagcaggagggtccggagtattgggacgaggagacaGggaAgtgaaggccctcacagactCaccgagtggacc
20 tggggaccctgcgcggctactacaaccagagcgaggccgggttctcacaccGtccagaGgatgtatggctgcgacgt
ggggctcggacTggcgcttccctccgcgggtaccaccagtagcctacgacggcaaggattacatcgccctgaaagag
gacctgcgctcttggaccgcgccggacatggcagctcagaccaccaagcacaagtgaggaggcgcccaatgTggcgg
agcagITgagagccctaccitggaggggcaCgtgcgtggagtggctccgcagataccitggagaacgggaaggagacgt
gcagcgcacgg (SEQ ID NO:60) ;

25 A*0247 :

gctctcacctccatgaggtaattcttcacatccgtgtcccgcccgccggggagccccgcttcatcgcagtggg
ctacgtggacgacacgcagttcgtgcgggtcgacagcgacgccgcgagccggaggatggagccgcggcgccgtgg

atagagcaggagggtccggaglatlgggacggggagacacggaaagtgaaggccactcacagaGlcaccgagtgg
acctggggacccitgcgcggtactacaaccagagcgaggccggttctcacacctccagaggaigtatggctgcga
cgtggggtcggactggcgcttcttgcgcggtaccaccagtagcctacgacggcaaggattacatcgccctgaaa
gaggacctgcgctcttggaccgcgcgagacatggcagc tcagaccaccaagcacaagtgggaggcggcccatgtgg
5 cggagcagtgagagccctacctggagggcacgtgcgtggagtggctccgcagatacctggagaacgggaaggagac
gctgcagcgcacgg (SEQ ID NO:61) ;

A*0248 :

gctctcactccatgaggatitcttccacatccgigtcccgcccgccgaggagccccgcttcatcgagtgagg
ctacgtggacgacacgcagltcgtgcggttcgacagcgacgccgagccagaggatggagccgccccgcccgtgg
10 atagagcaggaggggcccggaglatlgggacgaggagacAGggaaagtgaaggccactcacagactgaccgagtgg
acctggggacccitgcgcggtactacaaccagagcgaggccggttctcacacctccagaggaigtatggctgcga
cgtggggtcggactggcgcttcttgcgcggtaccaccagtagcctacgacggcaaggattacatcgccctgaaa
gaggacctgcgctcttggaccgcgcgagacatggcagc tcagaccaccaagcAcaagtgggaggcggcccatgTgg
cggagcagTgagagCctacctggagggcaCgtgcgtggagTggctccgcagatacctggagaacgggaaggagac
15 gctgcagcgcacgg (SEQ ID NO:62) ;

A*0249 :

gctctcactccatgaggatitcttccacatccgigtcccgcccgccgaggagccccgcttcatcgAgitggg
ctacgtggacgacacgcagltcgtgcggttcgacagcgacgccgagccagaggatggagccgccccgcccgtgg
atagagcaggagggtccggaglatlgggacGggagacacggaaAgitgaaggccactcacagactCaccgagtgg
20 acctggggacccitgcgcggtactacaaccagagcgaggccggttctcacaccGtccagaGgatgtatggctgcga
cgtggggtcggactggcgcttcttgcgcggtaccacCagTaccgctacgacggcaaggattacatcgccctgaaA
gaggacctgcgctcttggaccgcgcgagacatggcagc tcagaCaccaagcAcaagtgggaggcggcccatgTgg
cggagcagcggagagccctacctggagggcaCgtgcgtggagTggctccgcagatacctggagaacgggaaggagac
gctgcagcgcacgg (SEQ ID NO:63) ;

25 A*0250 :

gctccactccatgaggatitcttccacatccAtgtcccgcccgccgaggagccccgcttcatcgccgtggg
ctacgtggacgacacgcagltcgtgcggttcgacagcgacgccgagccagaggatggagccgccccgcccgtgg

atagagcaggagggcgaggatattggacggggagacacggaaAgigaaggcccactcacagactCaccgagtgga
accitggggacccitgcgcggctactacaaccagagcgaggccgggtctcacaccatccagaggatgtatggctgcga
cgtggggccggacgggcgcttctccgcggtaccaccagctacgcttacgacggcaaggattacatcgccctgaaa
gaggacctgcgctcttggaccgcgcgagacatggcagctcagaccaccaagcacaagtgaggaggcgcccatgttg
5 cggagcagtgagagccatccitggagggcacgtgcgtggagtggctccgcagataccitggagaacgggaaggagac
gtctcagcgccacgg (SEQ ID NO:64) ;

A*0251 :

gtcttcacitccatgaggatattctacacCtccgtgtcccggcccggccgaggagccccgttcaicgcagtgagg
ctacgtggacgacacgcagttcgtgcgggtcgacagcgacgccgcgagccagaggatggagccgcgggcgccgttg
10 atagagcaggaggggtccggagatattggacggggagacacggaaagigaaggcccactcacagactcaccgagtgga
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gaggacctgcgctcttggaccgcgcgagacatggcagctcagaccaccaagcAcaagtgaggaggcgcccatgttg
cggagcagttgagagccatccitggagggcaCgtgcgtggagTggctccgcagataccitggagaacgggaaggagac.
15 gtctcagcgccacgg (SEQ ID NO:65) ;

A*0252 :

gtcttcacitccatgaggatattctacacCtccgtgtcccggcccggccgaggagccccgttcaicgcagtgagg
ctacgtggacgacacgcagttcgtgcgggtcgacagcgacgccgcgagccagaggatggagccgcgggcgccgttg
20 atagagcaggaggggtccggagatattggacggggagacacggaaagigaaggcccactcacagactcaccgagtgga
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cgtgggggtcggacgggcgcttctccgcggtatgaAcagcagccctacgacggcaaggattacatcgccctgaaa
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cggagcagttgagagccatccitggagggcacgtgcgtggagtggctccgcagataccitggagaacgggaaggagac
gtctcagcgccacgg (SEQ ID NO:66) ;

25 A*0254 :

gtcttcacitccatgaggatattctacacCtccgtgtcccggcccggccgaggagccccgttcaicgcagtgagg
ctacgtggacgacacgcagttcgtgcgggtcgacagcgacgccgcgagccagaggatggagccgcgggcgccgttg

atagagcaggagggtccggagiat tgggacggggagacacggaaagtgaaggcccactcacagactcaccgagtgg
acc tggggaccc tgcgcggctactacaaccagagcgaggccggt tctcacaccGtccagaggaigtatggctgcga
cgtggggtcggactggcgcttctccgcggtaccaccagtagcctacgacggcaaggattacatcgccctgaaa
gaggacctgcgcctt tggaccgcgcggaatggcagctcagaccaccaagcAcaagtgggaggcgccca tTgg
5 cggagcagcAgagagcctacctggagggaCgtgcgtggacgggtccgcagatacctggagaacgggaaggagac
gctgcagcgcacgg (SEQ ID NO:67) ;

A*0255 :

gctctcactcca tgggta tttcttcacatccgtgtcccgcccgccgaggagccccgt tcatcgcatggg
ctacgtggacgacacgcagttcg tgcggttcgacagcgacgccgcgagccagaggatggagccgcgggcgccgtgg
10 atagagcaggaggggcccggagiat tgggaccggaaCacacggaaigtgaaggcccactcacagactCaccgagtgg
acctggggaccc tgcgcggctactacaaccagagcgaggccggt tctcacaccGtccagaGgatgtatggctgcga
cgtggggtcggactTggcgcttctccgcggtaccaCagTaccctacgacggcaaggattacatcgccctgaaaA
gaggacctgcgcctt tggaccgcgcggaatggcagctcagaCcaccaagcacaagtgggaggcgccca tTgg
cggagcagTtagagcctacctggagggaCgtgcgtggagTggctccgcagatacctggagaacgggaaggagac
15 gctgcagcgcacgg (SEQ ID NO:68) ;

A*0256 :

atggccgtcatggcgccccgaaccc tgc tcttctac tctcggggcTctggccctgaccagacctgggcgggct
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cgtggacgacacgcagttcg tgcggttcgacagcgacgccgcgagccagaggatggagccgcgggcgccgtggata
20 gagcaggagggtccggagiat tgggaccaggagacacggaa tgaaggcccaGtcacagactCaccgagtggacc
tggggaccc tgcgcggctactacaaccagagcgaggccggt tctcacaccGtccagaGgatgtatggctgcgacgt
ggggtcggactTggcgcttctccgcggtaccaccagtagcctacgacggcaaggattacatcgccctgaaagag
gacctgcgcctt tggaccgcgcggaatggcagctcagaccaccaagcacaaagtgggaggcgccca tTggcgg
agcagTtagagcctacctggagggaCgtgcgtggagtggtccgcagatacctggagaacgggaaggagacgt
25 gcagcgacggacgccccaaaacgcatatgactcaccacgtgtctctgacca tgaagccaccc tgggtgc tgg
gcccc tggcttctacctgcggagatcacactgacctggcagcggtatgggaggaccagaccaggacacggagc
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atagagcaggagggtccggagtaattgggacggggagacacggaaagtgaaggcccacacacagacac accgagtggt
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 cgtgggggtcggactggcgcttccctccgcggtaccaccagtagcctacgacggcaaggattacalc gccctgaaa
 gaggaccitgcgctcttggaccgcgcggaatggcagctcagaccaccaagcacaagtgggaggcggcccatgttg
 5 cggagcagittagagcctaccitggagggcacgtgcgtggagtggtccgcagataccitggagaacgggaaggagac
 gctgcagcgacggacgccccaaaacgcatatgactcaccacgctgtctctgaccatgaagccaccctgagggtgc
 tggggccctgagcttctaccctgcggagatcacactgacctggcagcgggatggggaggaccagaccaggacacgg
 agctcgtggagaccaggccitgcaggggatggaaccticcagaagtggcgggctgttggttggtccctctggacagga
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 10 NO:72) ;
 A*0260 :
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 15 accitggggaccctgcgcggctactacaaccagagcgaggccgggtctcacaccgtccagaggatgia tggctgcga
 cgtgggggtcggactggcgcttccctccgcggtaccaccagtagcctacgacggcaaggattacalc gccctgaaa
 gaggaccitgcgctcttggaccgcgcggaatggcagctcagaccaccaagcacaagtgggaggcggcccatgttg
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 gctgcagcgacgg (SEQ ID NO:73) ;
 20 A*030101 :
 atggccgtcatggcgccccgaacctccctctgtctactctcggggggccctggccctgaccagacct gggcgggct
 cccactccatgaggtaatttcttcacatccgtgtcccgcccgcccgaggagccccgcttcatcgc cgtgggctta
 cgtggacgacacgcagttcgtgcggttcgacagcgacgcccgagccagaggatggagccgcgggcgccgtggata
 gagcaggagggggcggtatitgggaccaggagacacggaaatggaaggcccaGtcacagactgacc gagitGacc
 25 tggggaccctgcgcggctactacaaccagagcgaggccgggtctcacaccatccagataatglatggctgcgacgt
 ggggtcggacggcgcttccctccgcggtaccggcaggacgctacgacggcaaggattacalcgcc ctgaacgag
 gaccitgcgctcttggaccgcgcggaatggcggctcagatcaccaagcgaagtgggaggcggccc atAgggcgg

agcagTTgagagcclaccTggaTggcacgTgcgTggagTggcTccgcagTaccTggagaacgggaaggagacgcT
gcagcgcacggaccccccaagacacataTgaccaccaccccaTcTcTgaccatgaggccacccTgaggTgcTgg
gcccTgggTcTcTaccTgcggagatcacacTgaccTggcagcgggaTggggaggaccagaccaggacacggagc
TcgTggagaccaggccTgcaggggaTggaacctTccagaagTggcgggcTgTggTggTgcTcTcTggagaggagca
5 gagatacacctTgcaTgTgcagcatgagggtcTgcccagccccTcacctTgagatgggag (SEQ ID

NO:74) ;

A*030102 :

gcTcccacTccatgaggTatTcTcTcacatccgTgTcccggcccgccgcggggagcccgcTcTcTcgcgTggg
cTaccTggacgacacgcagTcTgTgcggtTgcacagcgacccgcgagccagaggatggagccgcgggcgcgTgg
10 atagagcaggaggggcccggagTatTgggaccaggagacacggaatgTgaaggcccaGtcacagacTgaccgagTgG
acctggggacccTgcgcggcTactacaaccagagcgaggccggtTcTcacacatccagataatgTatggcTgcga
cgTggggtcggacgggcgcTcTcTccgcgggtaccggcaggacgcctacgacggcaaggattacatcgccctgaac
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cggagcagcTgagagcclaccTggaTggcacgTgcgTggagTggcTccgcagTaccTggagaacgggaaggagac
15 gcTgcagcgacgg (SEQ ID NO:75) ;

A*030103 :

gcTcccacTccatgaggTatTcTcTcacatccgTgTcccggcccgccgcggggagcccgcTcTcTcgcgTggg
cTaccTggacgacacgcagTcTgTgcggtTgcacagcgacccgcgagccagaggatggagccgcgggcgcgTgg
20 atagagcaggagggTccggagTatTgggaccaggagacacggaatgTgaaggcccaGtcacagacTgaccgagTgG
acctggggacccTgcgcggcTactacaaccagagcgaggccggtTcTcacacatccagataatgTatggcTgcga
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cggagcagcTgagagcclaccTggaTggcacgTgcgTggagTggcTccgcagTaccTggagaacgggaaggagac
gcTgcagcgacgg (SEQ ID NO:76) ;

25 A*0302 :

atggccgTcTatggcggccgaacctcTcTcTgTcTcTcTggggccctggccctgacccagaccTggcgggcT
cccacTccatgaggTatTcTcTcacatccgTgTcccggcccgccgcggggagccccgcTcTcTcgcgTgggcta

cgtaggacgacacgcagttcgtagcggttcgacagcgacgccgcgagccagaggatggagccgcgggcgccgtggat a
gagcaggagggggccggagtaattgggaccaggagacacggaaatgtaaggcccagtcacagactgaccgagtaggac c
tggggaccc tgcgcggctactacaaccagagcgaggccggtttcacacatccagataaigtatggctgcgacgt
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A*1103

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A*240203 :

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A*240302 :

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gctgcagcgacgg (SEQ ID NO:120) ;

A*2415 :

gctcccatccatgaggtatcttccacatccgtgtccggcccgccggggagccccgttcatcgccgtggg
ctacgtggacgacacgcagttcgtgcggttcgacagcgacgccgcgagccagaggatggagccgccccgttgg
25 atagagcaggagggccggagiatitggacgaggagacaGggaaagtgaggccctcacagactgaccgagaga
accitcggtatcggtctccgtactacaaccagagcgaggCgggttctcacacctccagatgatgtatggctgcga
cgtggggccggacgggcttctccgcgggtaccaccagTgcctacgacggcaaggattacatcgccctgaaA

gaggaccitgcgtctitggaccgcgccggacatggcGgctcagatcaccaagcgcaagtgaggaggcgcccatgtgg
cggagcagcAgagagCctaccitggagggcaCgtgctggacgggctccgcagataccitggagaacgggaaggagac
gctgcagcgacgg (SEQ ID NO:121) ;

A*2417 :

5 gctcccacttccatgaggtatitctccacatccgtgtcccggcccgccgaggagccccgttcatcgccgtggg
ctacgtggacgacacgcagttcgtgctgttcgacagcgacgccgagccagaggatggagccgaggcgccgtgg
atagagcaggagggccggagtattgggacgaggagacaGggaaagtgaaggcccacitacagactgaccgagaga
accitcggtatcgcgctcGctactacaaccagagcgaggCgggttctcacacctccagatgatgtTggctgcga
cgtggggTcggacgggcttctccgctgggtaccggcaggacgcttacgacggcaaggattacatcgccctgaaA
10 gaggaccitgcgtctitggaccgcgccggacatggcGgctcagatcaccaagcgcaagtgaggaggcgcccatgtgg
cggagcagcAgagagCctaccitggagggcaCgtgctggacgggctccgcagataccitggagaacgggaaggagac
gctgcagcgacgg (SEQ ID NO:122) ;

A*2418 :

gctcccacttccatgaggtatitctccacatccgtgtcccggcccgccgaggagccccgttcatcgccgtggg
15 ctacgtggacgacacgcagttcgtgctgttcgacagcgacgccgagccagaggatggagccgaggcgccgtgg
atagagcaggagggccggagtattgggacgaggagacagggaagtgaaggcccactacagactgaccgagaga
accitcggtatcgcgctccgtactacaaccagagcgaggccggttctcacacctccagatgatgtTggctgcga
cgtggggTcggacgggcttctccgctgggtaccaccagtacgcttacgacggcaaggattacatcgccctgaaA
gaggaccitgcgtctitggaccgcgccggacatggcGgctcagatcaccaagcgcaagtgaggaggcgcccatgAgg
20 cggagcagTTgagagcctaccitggaTggcagctgctggagtggctccgcagataccitggagaacgggaaggagac
gctgcagcgacgg (SEQ ID NO:123) ;

A*2419 :

gctcccacttccatgaggtatitctccacatccgtgtcccggcccgccgaggagccccgttcatcgccgtggg
ctacgtggacgacacgcagttcgtgctgttcgacagcgacgccgagccagaggatggagccgaggcgccgtgg
25 atagagcaggagggccggagtattgggacgaggagacaGggaaagtgaaggcccaGtccagactgaccgagtG
accitggggacctgcgctgtactacaaccagagcgaggacgggttctcacacctccagatgatgtTggctgcga
cgtggggTcggacgggcttctccgctgggtaccaccagTaccgttacgacggcaaggattacatcgccctgaaA

gaggacctgcgctcttggaccgcggcggacatggcGgctcagatcaccaagcgcaagtgggaggcggcccatgtgg
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gctgcagcgcacgg (SEQ ID NO:124) ;

A*2420 :

5 gctcccaatccatgaggtatttctccacatccgtgtccggcccgccggggagccccgcttcatcgccgtggg
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acctgcggatcgcgctcCgtactacaaccagagcgaggCgggttctcacacctccagatgatgtTggctgcga
cgtggggTcggacgggcgcttctccgcggtaccaccagTaccctacgacggcaaggattacatcgccctgaAA
10 gaggacctgcgctcttggaccgcggcggacatggcGgctcagatcaccaagcgcaagtgggaggcggcccatgtgg
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gctgcagcgcacgg (SEQ ID NO:125) ;

A*2421 :

gctcccaatccatgaggtatttctccacatccgtgtccggcccgccggggagccccgcttcatcgccgtggg
15 ctacgtggacgacacgcagttcgtgcggttcgacagcgacgccgcgagccagaggatggagccgcccgcgcgtgg
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acctgcggatcgcgctcCgtactacaaccagagcgaggCgggttctcacacctccagatgatgtTggctgcga
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gaggacctgcgctcttggaccgcggcggacatggcGgctcagatcaccaagcgcaagtgggaggcggcccatgtgg
20 cggagcagcAgagagCctacctggagggcaCgtgcgtggacgggtccgcagatacctggagaacgggaaggagac
gctgcagcgcacgg (SEQ ID NO:126) ;

A*2422 :

atggccgtcatggcgccccgaacctcgtcttgcctcctcggggccctggccctgaccagacctgggcaggct
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25 cgtggacgacacgcagttcgtgcggttcgacagcgacgccgcgagccagaggatggagccgcccgcgcgtggata
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NO:127) ;

A*2423 :

10 gctcccatccaatgaggtatttctccacatccgtgtcccgcccgccgaggaggagcccgcttcatcgccgtggg
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atagagcaggaggggcccggagtattgggacgaggagacaGggaaagtgaaggcccatcacagacigaccgagaga
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15 gaggacctgcgctcttggaccgcggcggacatggcggctcagatcaccaagcgcaagtgaggaggcgcccaigtgg
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gctgcagcgacgg (SEQ ID NO:128) ;

A*2424 :

gctcccatccaatgaggtatttctccacatccgtgtcccgcccgccgaggaggagcccgcttcatcgccgtggg
20 ctacgtggacgacacgcagttcgtgcggttcgacagcgacgccgagccagaggatggagccgaggcgccgtgg
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25 cggagcagTgagagCctacctggagggaCgtgcgtggacgggtccgcagatacctggagaacgggaaggagac
gctgcagcgacgg (SEQ ID NO:129) ;

A*2425 :

gctcccacttccatgagglGtttctccacatccgigtcccggcccggccgaggagccccgcttcatcgccgtggg
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5 cgtggggctggacggcgcttccctccgcggttaccaccaglacgcttacgacggcaaggattacatcgccctgaaa
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gctgcagcgacgg (SEQ ID NO:130) ;

A*2426 :

10 aaccttcttctgctacttctgggggcccgtggccctgacctagacctgggcaggctcccacttccatgaggtatttc
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NO:131) ;

A*2427 :

20 atggccgtcatggcgccccgaacctcgttctgctacttctgggggcccgtggccctgacctagacctgggcaggct
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25 ggggttcggacggcgcttccctccgcggttaccaccaglacgcttacgacggcaaggattacatcgccctgaaagag
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A*2428 :

gctcccacitccatgaggtatttctccacatccgtgtccggccccggccgaggagccccgttcatcgccgtggg
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5 atagagcaggagggccggaglatlgggacgaggagacaGggaaagtgaaggcccacitcacagacitaccgagtgG
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cggagcagcAgagagCctaccitggagggaCgtgcgtggacgggtccgcagataccitggagaacgggaaggagac
10 gctgcagcgacgg (SEQ ID NO:133) ;

A*2429 :

gctcccacitccatgaggtatttctccacatccgtgtccggccccggccgaggagccccgttcatcgccgtggg
ctacgtggacgacacgcagttcgtgcggttcgacagcgacgccgagccagaggatggagccgaggcgccgtgg
atagagcaggagggccggaglatlgggacgaggagacacggaaagtgaaggcccacitcacagacitaccgagaga
15 acctgcggtatcggtctCgttactacaaccagagcgaggCgggttctcacacctccagatgatgtTggctgcga
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gctgcagcgacgg (SEQ ID NO:134) ;

20 A*2430 :

gctcccacitccatgaggtatttctccacatccgtgtccggccccggccgaggagccccgttcatcgccgtggg
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gctgcagcgacgg(SEQ ID NO:135) ;

A*2431 :

gctcccatccatgaggtatttctccacatccgtgtccggcccgccggggagccccgcttcatcgccgtggg
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5 atagagcaggaggggcccggagttatgggacgagCagacagggaaagtgaaggcccacttcacagactgaccgagaga
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10 gctgcagcgacgg(SEQ ID NO:136) ;

A*2432 :

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15 Gcctgcggatcgcgtccgctactacaaccagagcgaggccggtttctcacacctccagatgatgtttggctgcga
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gctgcagcgacgg(SEQ ID NO:137) ;

20 A*2433 :

gctcccatccatgaggtatttctccacatccgtgtccggcccgccggggagccccgcttcatcgccgtggg
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tggggcc|tgagc|t|c|accc|tgcggagatcacac|gacc|tggcagcggga|ggggaggaccagaccaggacacgg
agc|cgt|ggagaccaggcc|tcaggggat|ggaacct|ccagaagt|ggg|ggc|gt|gg|gg|g|cc|t|c|ggacagga
gcagaga|acacc|tgc|at|gt|gcagca|tgagg|T|t|g|c|c|c|a|a|g|c|c|c|c|c|accc|t|g|a|g|t|ggg|(SEQ ID

5 NO:138) ;

A*2434 :

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c|acg|t|g|g|a|c|g|a|c|a|c|g|c|a|g|t|c|g|t|g|c|g|g|t|c|g|a|c|a|g|c|g|a|c|g|c|c|g|g|a|g|c|c|a|g|g|a|t|g|g|a|g|c|c|g|g|g|c|c|c|g|t|g|g|
a|t|a|g|a|g|c|a|g|g|a|g|g|g|c|c|g|g|a|g|t|a|t|g|g|g|a|c|g|a|g|g|a|c|a|g|g|g|a|a|a|g|t|g|a|a|g|g|c|c|c|a|c|t|c|a|c|a|g|a|t|g|a|c|c|g|a|g|a|g|a|
10 acc|tgc|gga|t|c|g|c|g|t|c|c|g|t|a|c|t|a|c|a|a|c|c|a|g|a|g|c|g|a|g|g|c|c|g|t|c|t|c|a|c|a|c|c|t|c|c|a|g|a|t|g|a|t|g|t|t|g|g|c|t|g|c|g|a|
c|g|t|g|g|g|t|c|g|g|a|c|g|g|g|c|g|t|t|c|t|c|c|g|c|g|g|t|a|c|c|a|c|c|a|g|t|a|c|g|c|t|a|c|g|a|c|g|g|c|a|a|g|g|a|t|a|c|a|t|c|g|c|c|t|g|a|a|
g|a|g|g|a|c|t|g|c|g|t|c|t|t|g|g|a|c|c|g|g|c|g|g|a|c|a|t|g|g|c|g|g|t|c|a|g|a|t|c|a|c|c|a|a|g|c|g|c|a|a|g|t|g|g|g|a|g|g|c|g|g|c|c|c|a|t|g|t|g|g|
c|g|g|a|g|c|a|g|c|A|g|a|g|a|g|c|t|a|c|t|t|g|g|a|g|g|c|a|c|g|t|c|g|t|g|g|a|c|g|g|c|t|c|g|c|a|g|a|t|a|c|t|t|g|g|a|a|c|g|g|g|a|a|g|g|a|g|a|c|
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15 A*2435 :

gc|ccccact|cca|tgagg|tat|t|c|ccacat|ccg|t|g|c|c|c|g|c|c|c|g|g|c|c|g|g|g|g|g|g|c|c|c|c|g|t|c|a|t|c|g|c|c|g|t|g|g|g|
c|acg|t|g|g|a|c|g|a|c|a|c|g|c|a|g|t|c|g|t|g|c|g|g|t|c|g|a|c|a|g|c|g|a|c|g|c|c|g|g|a|g|c|c|a|g|g|a|t|g|g|a|g|c|c|g|T|g|g|g|c|c|c|g|t|g|g|
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20 c|g|t|g|g|g|t|c|g|g|a|c|g|g|g|c|g|t|t|c|t|c|c|g|c|g|g|t|a|c|c|a|c|c|a|g|t|a|c|g|c|t|a|c|g|a|c|g|g|c|a|a|g|g|a|t|a|c|a|t|c|g|c|c|t|g|a|a|
g|a|g|g|a|c|t|g|c|g|t|c|t|t|g|g|a|c|c|g|g|c|g|g|a|c|a|t|g|g|c|g|g|t|c|a|g|a|t|c|a|c|c|a|a|g|c|g|c|a|a|g|t|g|g|g|a|g|g|c|g|g|c|c|c|a|t|g|t|g|g|
c|g|g|a|g|c|a|g|c|a|g|a|g|a|g|c|t|a|c|t|t|g|g|a|g|g|c|a|c|g|t|c|g|t|g|g|a|c|g|g|c|t|c|g|c|a|g|a|t|a|c|t|t|g|g|a|a|c|g|g|g|a|a|g|g|a|g|a|c|
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A*2437 :

25 gc|ccccact|cca|tgagg|tat|t|c|ccacat|ccg|t|g|c|c|c|g|c|c|c|g|g|c|c|g|g|g|g|g|g|c|c|c|c|g|t|c|a|t|c|g|c|c|g|t|g|g|g|
c|acg|t|g|g|a|c|g|a|c|a|c|g|c|a|g|t|c|g|t|g|c|g|g|t|c|g|a|c|a|g|c|g|a|c|g|c|c|g|g|a|g|c|c|a|g|g|a|t|g|g|a|g|c|T|g|c|g|g|g|c|c|c|g|t|g|g|
a|t|a|g|a|g|c|a|g|g|a|g|g|g|c|c|g|g|a|g|t|a|t|g|g|g|a|c|g|a|g|g|a|c|a|g|g|g|a|a|a|g|t|g|a|a|g|g|c|c|c|a|c|t|c|a|c|a|g|a|t|g|a|c|c|g|a|g|a|g|a|

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5 gctgcagcgacgg(SEQ ID NO:141) ;

A*2438 :

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10 accatgcggatcgcgtccgctactacaaccagagcgaggccggtctcacacccctccagatgaltgttggctgcga
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15 A*2501 :

atggcgtcatggcgccccgaacccctgttctgtctactctcgggggccctggccctgaccagacctgggcgggct
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25 gccctgagcttctacccatgcggagatcacactgacctggcagcgggatgggaggaccagaccaggacacggagc
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NO:143) ;

A*2502 :

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5 cgtggacgacacgcagttcgtgcggttcgacagcgacgcccgagccagaggatggagccgcccggcgccgtggata
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15 NO:144) ;

A*2503 :

gtccccactccatgaggtatcttccacatccgtgtcccgcccgcccggggagccccgcttcatcgccgtggg
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25 A*2504 :

gtccccactccatgaggtatcttccacatccgtgtcccgcccgcccggggagccccgcttcatcgccgtggg
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5 cggagcagcAgagagcctaccitggagggccgggtgcgtggagTggctccgcagataccitggagaacgggaaggagac
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A#2601 :

alggccgicalggcggccgaaccctcgctcgtctacitcggggggccctggccctgaccagacctgggcgggct
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10 cgtggacgacacgcagittcgtgcggttcgacagcgacgccgcgagccagaggatggagccgcggcgccgtggata
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15 agcagTggagagcctaccitggagggccgggtgcgtggagtggctccgcagataccitggagaacgggaaggagacgt
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20 NO:147) ;

A#2602 :

alggccgicalggcggccgaaccctcgctcgtctacitcggggggccctggccctgaccagacctgggcgggct
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25 gagcaggaggggcccggagtatlgggaccggaacacacggaatgigaaggccacacagactgaccgagcgaacc
tggggaccttgcgcggctactacaaccagagcgaggacgggttctacaccatccagaggaigtalggctgcgacgt
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5 tctggagaccaggccctgcagggaatgggacctccagaagtggcgctctgtgggtggttctctggacaggagca
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NO:148) ;

A*2603 :

atggccgtcatggcgccccgaacctcgtctctgtactctcgggggcccggccctgaccagacctggcggggt
10 cccactccatgaggtatttctacacctccgtgtccggcccgccgaggagccccgcitcatcgccgtgggcta
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15 gacctgcgtcttggaccgcgccggacatggcggcicagatcaccagcgcaagtgggagacggcccatgaggcgg
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20 gagatcacctgccatgtgcagcatgagggtctgccaagccccaccctgagatgggag (SEQ ID
NO:149) ;

A*2604 :

atggccgtcatggcgccccgaacctcgtctctgtactctcgggggcccggccctgaccagacctggcggggt
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25 cgtggacgacacgcagttcgtgcggttcgacagcgacgccgcgagccagaggatggagccgccccgcccgtggata
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NO:150) ;

A*2605 :

10 atggccgctatggcggccgaacctcgtcttgctactctcgggggccctggccctgacctgggcgggct
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20 tcgtggagaccaggccctgcagggaaggGacctccagaagtggcgctctggtggctgctctggacaggagca
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NO:151) ;

A*2606 :

25 gctcccactccaatgaggtaattctacacctccgtgtccggccggccggggagccccgcttcatcgccgtggg
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5 A*2607 :

aaggccgtcatggcgccccgaacccctcgtccctgctactctcgggggccctggccctgaccagacctgggcgggct
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10 tggggacccctgcgcggctactacaaccagagcgaggacggctctcacaccatccagaggatgtatggctgcgacgt
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NO:153) ;

A*2608 :

20 aaggccgtcatggcgccccgaacccctcgtccctgctactctcgggggccctggccctgaccagacctgggcgggct
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25 gggggccggacgggcgcttccctcgcggggtaccagcaggacgcttacgacggcaaggattacatcgccctgaacgag
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A*2609 :

gtccccactccatgaggtatitctacacctccgtgtcccgccccggccgccccgagccccgttcatcgccgtggg
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atagagcaggagggggccggaglat tgggaccggaacacacggaatgtgaagggccactcacagactgaccgagcga
10 acctggggaccttgcgcggctactacaaccagagcgaggacggttctcacaccatccagaggatgtatggctgcga
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15 A*2610 :

gtccccactccatgaggtatitctacacctccgtgtcccgccccggccgccccgagccccgttcatcgccgtggg
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20 cgtggggccggacgggcgttccctccgcgggtaccagcaggacgcttacgacggcaaggattacatcgccctgaaA
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A*2612 :

25 gtccccactccatgaggtatitctacacctccgtgtcccgccccggccgccccgagccccgttcatcgccgtggg
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A*2613 :

gctcccatccatgaggtaattctacacctccgtgtcccgccccggccgcgaggagccccgcttcatcgccgtggg
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15 A*2614 :

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A*2615 :

25 atggccgctatggcggccgaacccctgctccgtgctactctcgggggccctggccctgacccagacctggcgggct
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5 agcag tggagagcct acc tggaggccgg tgcgtggag tggc tccgcagat acc tggagaacgggaaggagacgct
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10 NO:160) ;
A*2616 :
gc tccac tccatgaggat t tct tccacatccgt tcccgcccgccgaggagccccgc t tca tgc cgtggg
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atagagcaggagggccggagiat tgggaccggaacacacggaatgtgaaggcccac tcaagac taccgagcga
15 acctggggaccc tgcgcggc taciacaaccagagcgaggacgggt tctcacacatccagaggatgtatggc tgcga
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gaggacctgcgc tct tggaccgcgcggaatggcggc tcaatcaccagcgcaagtgggagAcggcccatgAgg
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20 A*2617 :
gc tccac tccatgaggat t tct tccacatccgt tcccgcccgccgaggagccccgc t tca tgc cgtggg
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atagagcaggagggccggagiat tgggaccggaacacacggaatgtgaaggcccac tcaagac taccgagcga
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25 cg tggggccggacgggcgct tcc tccgcggt acccagcaggacgct taccgagcgaaggattacatcgccctgaac
gaggacctgcgc tct tggaccgcgcggaatggcggc tcaatcaccagcgcaagtgggagacggcccatgagg
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gctgcagcgacgg (SEQ ID NO:162) ;

A*2618 :

gctcccacitccatgaggtaattctacacctccgltcccggcccgccgaggagccccgcttcatcgccgtggg
ctacgtggacgacacgcagttcgtgcggttcgacagcgacgccgcgagccagaggatggagccgcgggcgccgtgg
5 atagagcaggaggggcccggagtaattgggaccggaacacacggaatgtgaaggccactcacagactgaccgagcga
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10 gctgcagcgacgg (SEQ ID NO:163) ;

A*29010101 :

atggccgtcatggcgccccgaaccttcttctgclactcttgggggcccggccctgacctgagccagacctgggcgggct
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NO:164) ;

25 A*2902 :

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tggggacccitgcgcggctactacaaccagagcgaggccggt t c t c a c a c c a t c c a g a t g a t g t a t g g c t g c g a c g t
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5 g a c c t g c g c t c t t g g a c c g c g g c g g a c a t g g c g g c t c a g a t c a c c c a g c g c a a g t g g g a g g c g g c c c g t g t g g c g g
a g c a g t t g a g a g c c t a c c t g g a g g g c a c g t g c g t g g a g t g g c t c c g c a g a t a c c t g g a g a a c g g g a a g g a g a c g c t
g c a g c g c a c g g a c g c c c c a a g a c g c a t a t g a c t c a c c a c g c t g t c t c t g a c c a t g a g g c c a c c c t g a g g t g c t g g
g c c c t g a g c t t c t a c c c t g c g g a g a t c a c a c t g a c c t g g c a g c g g g a t g g g g a g g a c c a g a c c a g g a c a c g g a g c
t t g t g g a g a c c a g g c c t g c a g g g a t g g a a c c t t c c a g a a g t g g g c g t c t g t g g t g g t g c c t t c t g g a C a g g a g c a
10 g a g a t a c a c c t g c c a t g t g c a g a t g a g g g t c t g c c c a a g c c c c t a c c c t g a g a t g g g a g (SEQ ID
NO:165) ;

A*2903 :

atggccgtcatggcgccccgaaccttcttctgtctactcttgggggccc tggccc t g a c c c a g a c c t g g c c g g g c t
cccacttccatgaggtatttcaccacatccgtgtcccggcccggccgcggggagccccgcttca t c g c c g t g g g c t a
15 c g t g g a c g a c a c g c a g t t c g t g c g g t t t g a c a g c g a c g c c g c g a g c c a g a g g a t g g a g c c g c g g g c A c c g t g g a t a
g a g c a g g a g g g g c c g g a g t a t t g g g a c c t g c a g a c a c g g a a t g t g a a g g c c c a g t c a c a g a c t g a c c g a g c g a a c c
t g g g g a c c c t g c g c g g c t a c t a c a a c c a g a g c g a g g c c g g t t c t c a c a c c a t c c a g a t g a t g t a t g g c t g c g a c g t
g g g g t c g g a c g g g c g t t c c t c c g c g g g t a c c g g c a g g a c g c c t a c g a c g g c a a g g a t t a c a t c g c c t t g a a c g a g
g a c c t g c g c t c t t g g a c c g c g g c g g a c a t g g c g g c t c a g a t c a c c c a g c g c a a g t g g g a g g c g g c c c g t g t g g c g g
20 a g c a g t t g a g a g c c t a c c t g g a g g g c a c g t g c g t g g a c g g g c t c c g c a g a t a c c t g g a g a a c g g g a a g g a g a c g c t
g c a g c g c a c g g a c g c c c c a a g a c g c a t a t g a c t c a c c a c g c t g t c t c t g a c c a t g a g g c c a c c c t g a g g t g c t g g
g c c c t g a g c t t c t a c c c t g c g g a g a t c a c a c t g a c c t g g c a g c g g g a t g g g g a g g a c c a g a c c a g g a c a c g g a g c
t t g t g g a g a c c a g g c c t g c a g g g a t g g a a c c t t c c a g a a g t g g g c g t c t g t g g t g g t g c c t t c t g g a C a g g a g c a
g a g a t a c a c c t g c c a t g t g c a g a t g a g g g t c t g c c c a a g c c c c t a c c c t g a g a t g g g a g (SEQ ID
25 NO:166) ;

A*2904 :

gctcccacttccatgaggtatttcaccacatccgtgtcccggcccggccgcggggagccccgcttca t c g c c g t g g g

ctacgtggacgacacgcagttcgtgcgggttgacagcgacgccgcgagccagaggatggagccgcgggcaccgtgg
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acctggggacccigcgcggctactacaaccagagcgaggccggtttctcacaccaatccagatgatgtatggctgcga
cgtggggtcggacgggcgttccctccgcggtaccggcaggacgcctacgacggcaaggattacatcgccittgaac
5 gaggacctgcgctcttggaccgcggcggacatggcggctcagatcacccagcgcaagtgggaggcggcccGtgtgg
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A*2905 :

gctcccactccaatgaggtatttaccacatccgtgtcccgcccgccgcggggagccccgcttcatcgccgtggg
10 ctacgtggacgacacgcagttcgtgcgggttgacagcgacgccgcgagccagaggatggagccgcgggcAccgtgg
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acctggggacccigcgcggctactacaaccagagcgaggccggtttctcacaccaatccagatgatgtatggctgcga
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gaggacctgcgctcttggaccgcggcggacatggcggctcagatcacccagcgcaagtgggaggcggcccatgagg
15 cggagcagcAgagagccataccggagggcacgtgcgtggagTggctccgcagataccggagaacgggaaggagac
gctgcagcgacgg (SEQ ID NO:168) ;

A*2906 :

gctcccactccaatgaggtatttaccacatccgtgtcccgcccgccgcggggagccccgcttcatcgccgtggg
ctacgtggacgacacgcagttcgtgcgggttgacagcgacgccgcgagccagaggatggagccgcgggcAccgtgg
20 atagagcaggaggggcccggagtattgggacctgcagacacggaaigtgaaggcccagtcacagactgaccgagcga
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25 gctgcagcgacgg (SEQ ID NO:169) ;

A*2907 :

gctcccactccaatgaggtatttaccacatccgtgtcccgcccgccgcggggagccccgcttcatcgccgtggg

ctacgiggacgacacgcagttcgtgcggtttgacagcgacgccgcgagccagaggatggagccgcgggcAccgtgg
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5 gaggacctgcgctcttggaccgcggcggacatggcggctcagatcaccagcgcaagiggaggcgggcccggtgtgg
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gctgcagcgacgg (SEQ ID NO:170) ;

A*3001 :

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15 gacctgcgctcttggaccgcggcggacatggcggctcagatcaccagcgcaagt gggaggcgggcccgTgggcgg
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tcgtggagaccaggctgcaggggatggaacctccagaagtggcggtgtgtgtgggtggttcttggagaggagca
20 gatatacctgccatgtgcagcatgagggtctgcccagccctcacctgagatgggag (SEQ ID
NO:171) ;

A*3002 :

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25 cgtggacgacacgcagttcgtgcggttcgacagcgacgccgcgagccagaggatggagccgcgggcgccgtggata
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gcagcgacggaccccccaagacacataigaccaccaccccaictctgaccatgaggccacctgaggtgctgg
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NO:172) ;

A*3003 :

10 ggctcccatccatgaggtatttctccacatccgtgtcccgcccggcagtgAgagccccgcttcatcgcatggg
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aacctggggacccctgcgcggctactacaaccagagcgaggccggttctcacacatccagataatgtatggctgcg
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15 cgaggacctgcgcctctggaccgcgccggacatggcggctcagatcaccagcgcaagtgggaggcgcccgctCgg
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20 agcagag (SEQ ID NO:173) ;

A*3004 :

gcctcccatccatgaggtatttctccacatccgtgtcccgcccggcagtgAgagccccgcttcatcgcatggg
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atagagcaggagaggcctgagataggaccaggagacacggaatggaaggccctcacagactgaccgagaga
25 acctggggacccctgcgcggctactacaaccagagcgaggccggttctcacacatccagataatgtatggctgcga
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A*3006 :

gctcccacitccatgaggtatttctccacatccgtgtcccgcccggcagtgagagccccgttccatcgCagtggg
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gaggacctgcgctcttggaccgcgccggacatggcggtcagatcaccagcgcaagtgggaggcgcccatgtgg
10 cggagcagtgagagccctaccctggagggcacgtgcgtggagTggctccgcagataccctggagaacgggaaggagac
gctgcagcgacgg (SEQ ID NO:175) ;

A*3007 :

gctcccacitccatgaggtatttctccacatccgtgtcccgcccggcagtgagagccccgttccatcgCagtggg
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15 atagagcaggagagggcctgagtattgggaccaggagacagggaaAgigaaggccctcacagactgacCgagaga
accctggggacccctgcgcggctactacaaccagagcgaggccggttctcacaccaaccagataaigtatggctgcga
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20 gctgcagcgacgg (SEQ ID NO:176) ;

A*3008 :

atggccgtcatggcgccccgaaccttcttctgtctacitcggggggccctggccctgaccagacctggcggggt
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25 gagcaggagagggcTgagtattgggaccaggagacacggaaigtgaaggccctcacagactgaccgagtggacc
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gcagcgcacggaccccccaagacacataatgaccaccaccccaatctctgacataggccacccitagggtgcitgg
gcccitgggcttctacctgcggagatcacactgacctggcagcgggatggggaggaccagaccaggacacggagc
5 tctggagaccaggccitcaggggatggaacctccagaagtgggcggctgttggtggcttcttggagaggagca
gagatacaccitgccaatgtgcagcatgagggtctgccaagccccctacccitgagatgggag (SEQ ID
NO:177) ;

A*3009 :

gtctccacttccatgaggatattctccacatccgtgtcccgcccggcagtgAgagccccgcttcaatgcagitggg
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acctggggacccitgcgcggctactacaaccagagcgaggccggttctcacaccatccagataatgtatggctgcga
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15 cggagcagTtagagcctaccitggagggcacgtgcgtggagTggctccgcagataccitggagaacgggaaggagac
gtctcagcgcacgg (SEQ ID NO:178) ;

A*3010 :

gtctccacttccatgaggatattctccacatccgtgtcccgcccggcagtgagagccccgcttcaatgcagitggg
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20 atagagcaggagaggccitgagtattgggaccaggagacacggaaigtgaaggccctcacagactgaccgagaga
acctggggacccitgcgcggctactacaaccagagcgaggccggttctcacaccatccagataatgtatggctgcga
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25 gtctcagcgcacggaccccccaagacacataatgaccaccaccccaatctctgacataggccacccitagggtgc
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gcagagatacaccitgccatgtgcagcatgagggctcgcccaagccccicacccitgagatggg (SEQ ID
NO:179) ;

A*3011 :

gctcccactccaatgaggtatttctccacatccgtgtcccgcccgccagtgagagccccgttcatcgcagtggg
5 ctacgtggacgacacgcagttcgtgcggctcgacagcgacgcccgagccagaggatggagccgccccgcccgtgg
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accitggggacccitgcgcggctactacaaccagagcgaggccggtttcacacatccagataatgtatggctgcga
cgtggggctcggacggcgcttccitccgcggtatgaacagcacgcctacgacggcaaggattacatcgccctgaac
gaggacctgcgctcttggaccgccccggacatggcggtcagatcaccagcgcaagtgggagggcgccccgtTggg
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A*3012 :

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15 atagagcaggagaggccTgagtattgggaccaggagacacggaaatgtgaagggccacacagactgaccgagaga
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NO:181) ;

25 A*310102 :

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NO:182) ;

A*3102 :

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A*3103 :

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A*3104 :

alggccgtcatggcgccccgaaccctccctcgtctacTcTlggggccctggccctgaccagaccTggcgggct
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A*3105 :

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25 gctgcagcgacgg (SEQ ID NO:186) ;

A*3106 :

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A*3107 :

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A*3108 :

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25 gctgcagcgacgg(SEQ ID NO:189) ;

A*3109 :

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A*3201 :

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15 gacctgcgctcttggaccgcccgggacatggcggctcagatcaccagcgcaagtgggaggcgcccggtgtggcgg
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NO:191) ;

A*3202 :

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25 cgtggacgacacgcagttcgtgcggtttgacagcgacgccgcgagccagaggatggagccgcccggcgccgtggata
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A*3203 :

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A*3204 :

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20 ctacgtggacgacacgcagttcgtgcggttcgacagcgacgccgcgagccagaggatggagccgcgggcgccgtgg
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25 cggagcagttgagagcctacctggaTggcaCgtgcgtggagTggctccgcagatacctggagaacgggaaggagac
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A*3205 :

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5 tgcggatcgcgctccgctacttacaaccagagcgaggccggttctcacaccatccagatgatgtatggctgcgacgt
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A*3206 :

15 gctcccactccatgaggtaattcttcacatccgtgtccggccccggccggggagccccgcttcatcgccgiggg
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A*3207 :

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5 A*3301 :

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NO:198) ;

A*3303 :

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5 NO:199) ;

A*3304 :

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15 A*3305 :

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A*3306 :

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cggagcagttgagagccctacgtggaggcgacgtgcgtggagtggtccgcagatacctggagaacgggaaggagac
5 gctgcagcgacggaccccccaagacgcataatgactcaccacgcgtctctgaccaataggccaccctgaggtgc
tggggcctgagcttctacccigcggagatcacactgacctggcagcgggatggggaggaccagaccaggacacgg
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A*3401 :

atggccatcatggcggccgaacctcgtcttgcctacitcggggggccctggccctgaccagacctgggcgggct
10 cccactccatgaggtatttctacacctccgtgtccggcccgccgaggagccccgcttcatcgccgtgggctta
cgtggacgacacgcagttcgtgcggttcgacagcgacgccgcgagccagaggatggagccgcgggcgccgtggata
gagcaggagggggccggagtattgggaccggaacacacggaaagtgaaggcccgagtcacagactgaccgagtggaac
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ggggccggacggcgcttcciccgcggtaccAgcaggacgcttacgacggcaaggattacatcgccctgaacgag
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tctgtggagaccaggcctgcaggggatggaacctccagaagtggcgTctgtgtgtgtgcttctggaCaggagca
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NO:203) ;

A*3402 :

atggccgtcatggcggccgaacctcgtcttgcctacitcggggggccctggccctgaccagacctgggcgggct
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25 cgtggacgacacgcagttcgtgcggttcgacagcgacgccgcgagccagaggatggagccgcgggcgccgtggata
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5 gcccitgagcttctacccitgcggagatcacactgaccitggcagcgggatggggaggaccagaccaggacacggagc
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NO:204) ;

A*3403 :

10 gctcccacttccatgaggtaattctacacctccgtgtcccgcccgccggggagccccgttcatcgccgtggg
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15 gaggacctgcgtcttggaccgcgccggacatggcggctcagatcaccagcgcaagtgggagggcccatgAgg
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A*3404 :

gctcccacttccatgaggtaattctacacctccgtgtcccgcccgccggggagccccgttcatcgccgtggg
20 ctacgtggacgacacgcagttcgtgcggttcgacagcgacgcccgagccagaggatggagccgccccgcccgtgg
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gaggacctgcgtcttggaccgcgccggacatggcggctcagatcaccagcgcaagtgggagacggcccatgAgg
25 cggagcagTgagagcctaccitggagggcacgtgcgtggagTggctccgcagatacctggagaacgggaaggagac
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A*3405 :

gctcccacitccatgaggtatitctacacctccgigtcccgcccgccgaggagccccgcttcatcgccgtggg
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5 cgtggggccggacggcgcttccitccgcggttaccagcaggacgcttacgacggcaaggattacatTccctgaac
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A*3601 :

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gcccitgggtttctaccttgcggagatcacactgacctggcagcgggaiggaggaggaccagaccaggacacggagc
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NO:208) ;

A*3602 :

gctcccacitccatgaggtatitcttccatccgtgtcccgcccgccgaggagccccgcttcatcgccgtggg
25 ctacgtggacgacacgcagttcgtgcggttcgacagcgacgccgcgagccagaagatggagccgccccgcccgtgg
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5 A*3603 :

atggccgcatggcggccgaacccctccctcgtactctcggggggccctggccctgaccagaccctggcgggct
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gagcaggagggggccggagiatgggaccaggagacacggaatatgaaggcccatcacagacgaccgagcgaacc
10 tggggaccctgcgcggctactacaaccagagcaggacggttctcacaccCtccagatgatgtatggctgcgacgt
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NO:210) ;

A*3604 :

20 gctcccactccatgaggatattcttcacatccgtgtccggcccgccggggagccccgcttcatcgccgtggg
ctacgtggacgacacgcagttcgtgcggttcgacagcgacgccgagccagaagatggagccgcgggcgccgtgg
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25 gaggacctgcgccttggaccgcgcgacatggcagctcagatcaccaagcgcaagtgggaggcggtccatgcgg
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A*4301 :

atggccgtcatggcgccccgaacctcgtccctgctactctcggggggccctggccctgacctagacctgggcgggct
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cgtggacgacacgcagttcgtgcggttcgacagcgacgccgcgagccagaggatggagcccgggcgccgtggata
5 gagcaggagggggccggagttatgggaccTgcagacacggaatgtgaaggccctcacagactgacctgagcgaacc
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tcgtggagaccaggcctgcaggggatggGaccttccagaagtgggcgtctgtgggtggcttcttggacaggagca
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NO:212) ;

15 A*6601 :

atggccgtcatggcgccccgaacctcgtccctgctactctcggggggccctggccctgacctagacctgggcgggct
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20 tggggaccttgcgcggctactacaaccagagcgaggacggtttcacaccatccagaggatgtatggctgcgacgt
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NO:213) ;

A*6602 :

atggccgtcatggcggccgaacccctcgtccgtctacitcggggggccclggcccigaccagacctggcggggt
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5 cgtggacgacacgcagltcgtgcggttcgacagcgacccgagccagaggatggagccgcccggcgccgtggata
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10 agcagtgagagccctacctggagggcgAgctgcgtggagtggctccgcagatacctggagaacgggaaggagacgt
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gagataaccttgccatgtgcagcatgagggtctgccaagccccctacccctgagatggggag (SEQ ID

15 NO:214) ;

A*6603 :

gtccccactccatgaggiaitctacaccccggtgtccggcccgccggggagccccgtlcatcgccgtggg
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atagagcaggagggggccggagiatgggaccggaacacacggaatgtgaaggcccactcacagactgaccgagtg
20 acctggggacccctgcgcccgtactacaaccagagcgaggccggttctcacacatccagaggatglatggctgcga
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25 A*6604 :

gtccccactccatgaggiaitctacaccccggtgtccggcccgccggggagccccgtlcatcgccgtggg
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5 cggagcagtgagagcctaccigggagggccggctgcgtggagtggctccgcagaCacctggagaacgggaaggagac
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A*680101 :

atggccgtcatggcgccccgaacccctgctcctgctactctcggggggccctggccctgaccagacctgggcgggct
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10 cgtggacgacacgcagltcgtgcggttcgacagcgacgcccgagccagaggatggagccgcgggcgccgtggata
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tctgtggagaccaggccigcaggggaiggaaccttccagaagtgggTggctgtgggtggcttctggacaggagca
gagatacaccigccatgtgcagcatgagggtTigcccaagccctcacctgagatgggag (SEQ ID
20 NO:217) ;

A*680102 :

atggccgtcatggcgccccgaacccctgctcctgctactctcggggggccctggccctgaccagacctgggcgggct
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25 gagcaggagggggccggagiatlgggaccggaacacacggaatgigaaggccaGtcacagacigaccgagtggaac
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g c c c t g a g c t t c t a c c c t g c g g a g a t c a c a c t g a c c t g g c a g c g g g a t g g g g a g g a c c a g a c c c a g g a c a c g g a g c
5 t c g t g g a g a c c a g g c c t g c a g g g a t g g a a c c t t c c a g a a g t g g g T g g c t g t g g t g g t g c c t t c t g g a c a g g a g c a
g a g a t a c a c c t g c c a t g t g c a g c a t g a g g g t T i g c c c a a g c c c c t a c c c t g a g a t g g g a g (S E Q I D
N O : 2 1 8) ;

A*6802 :

a t g g c c g t c a t g g c g c c c c g a a c c c t c g t c c t g c t a c t c t c g g g g c c c t g g c c c t g a c c c a g a c c t g g g c g g g c t
10 c c c a c t c c a t g a g g t a t t c t a c a c c t c c A t g t c c c g g c c c g g c c g g g g a g c c c c g t t c a t c g c c g t g g g c t a
c g t g g a c g a c a c g c a g t t c g t g c g g t t c g a c a g c g a c g c c g c g a g c c a g a g g a t g g a g c c g c g g g c g c c g t g g a t a
g a g c a g g a g g g g c c g g a g t a t t g g g a c c g g a a c a c a c g g a a t g t g a a g g c c c a g t c a c a g a c t g a c c g a g t g g a c c
t g g g g a c c c t g c g c g g c t a c t a c a a c c a g a g c g a g g c c g g t t c t c a c a c c a t c c a g a g g a t g t a t g g c t g c g a c g t
g g g g c c g g a c g g g c g c t t c c t c c g c g g t a c c a c c a g t a c g c c t a c g a c g g c a a g g a t t a c a t c g c c c t g a a a g a g
15 g a c c t g c g c t c t t g g a c c g c g g c g g a c a t g g c a g c t c a g a c c a c c a a g c a c a a g t g g g a g g c g g c c c a t g t g g c g g
a g c a g t g g a g a g c c t a c c t g g a g g g c a c g t g c g t g g a g t g g c t c c g c a g a t a c c t g g a g a a c g g g a a g g a g a c g c t
g c a g c g c a c g g a c g c c c c c a a a c g c a t a t g a c t c a c c a c g c t g t c t c t g a c c a t g a a g c c a c c c t g a g g t g c t g g
g c c c t g a g c t t c t a c c c t g c g g a g a t c a c a c t g a c c t g g c a g c g g g a t g g g g a g g a c c a g a c c c a g g a c a c g g a g c
t c g t g g a g a c c a g g c c t g c a g g g a t g g a a c c t t c c a g a a g t g g g t g g c t g t g g t g g t g c c t t c t g g a c a g g a g c a
20 g a g a t a c a c c t g c c a t g t g c a g c a t g a g g g t T i g c c c a a g c c c c t a c c c t g a g a t g g g a g (S E Q I D
N O : 2 1 9) ;

A*680301 :

a t g g c c g t c a t g g c g c c c c g a a c c c t c g t c c t g c t a c t c t c g g g g c c c t g g c c c t g a c c c a g a c c t g g g c g g g c t
c c c a c t c c a t g a g g t a t t c t a c a c T i c c g t g t c c c g g c c c g g c c g g g g a g c c c c g t t c a t c g c c g t g g g c t a
25 c g t g g a c g a c a c g c a g t t c g t g c g g t t c g a c a g c g a c g c c g c g a g c c a g a g g a t g g a g c c g c g g g c g c c g t g g a t a
g a g c a g g a g g g g c c g g a g t a t t g g g a c c g g a a c a c a c g g a a t g t g a a g g c c c a c t c a c a g a c t g a c c g a g t g g a c c
t g g g g a c c c t g c g c g g c t a c t a c a a c c a g a g c g a g g c c g g t t c t c a c a c c a t c c a g a t g a t g t a t g g c t g c g a c g t

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NO:220) ;

A*680302 :

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A*6804 :

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A*6805 :

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A*6807 :

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A*6808 :

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A*6809 :

15 gctcccactccatgaggtaattctacacTtccgigtcccgccccggccgccccgagccccgcttcatcgccgtggg
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A*6810 :

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5 A*6812 :

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A*6813 :

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A*6814 :

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A*6815 :

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A*6816 :

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A*6817 :

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15 A*6819 :

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A*6820 :

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A*6821 :

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15 A*6822 :

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NO:238) ;

A*6823 :

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A*6901 :

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NO:240) ;

25 A*7401 :

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NO:241) ;

A*7402 :

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tggggacccitgcgcggctactacaaccagagcgaggccgggttctcacaccatccagatgatgtatggctgcgacgt
ggggccggacgggcgcttctccgcgggtaccAgcaggacgcciacgacggcaaggattacatcgccTigaacgag
gacctgcgctcttggaccgcggcggacatggcggctcagatcaccagcgcaagtgggaggcgcccggtgtggcgg
20 agcagttgagagcctacctggagggcacgtgcgtggagTggctccgcagatacctggagaacgggaaggagacgct
gcagcgacgg (SEQ ID NO:242) ;

A*7403 :

atggccgtcatggcgccccgaaccttcttctgtactcttggggggccctggccctgaccagaccaggcgggct
cccactccatgaggtaattcttcacatccgtgtcccgccccggcggggagccccgcttcatcgccgtgggcta
25 cgtaggacgacacgcagttcgtgcggtttgacagcgacgccgcgagccagaggatggagccgcggcgccgtggata
gagcaggagggggccggagttatgggaccaggagacacggaatgtgaaggccactcacagactgaccgagtaggacc
tggCgacccitgcgcggctactacaaccagagcgaggccgggttctcacaccatccagatgatgtatggctgcgacgt

ggggccggacgggcgcctccctccgcggtaccagcaggacgcctacgacggcaaggattacatcgccitgaacgag
gacctgcgctcttggaccgcggcgacatggcggctcagatcaccagcgcaagtgaggaggcgcccggtgtggcgg
agcagiltgagagcctacctggagggcacgtgcgtggagtggtccgcagatacctggagaacgggaaggagacgct
gcagcgcacgg (SEQ ID NO:243) ;

5 A*7404 :

ggctcccactccatgaggtaattcttcacatccgtgtcccgcccgccgaggagccccgcttcatcgccgtgg
gtacgtggacgacacgcagttcgtgcgggttgacagcgacgccgcgagccagaggatggagccgcggcgccgtg
gatagagcaggaggggtccggagtattgggaccgggagacacggaaAgtagaggccacacacagactgaccgagt
Gacctggggaccctgcgcggctactacaaccagagcgaggccggttctcacaccaaccagatgatgtatggctgcg
10 acgtggggccggacgggcgcCtccctccgcggtaccagcaggacgcctacgacggcaaggattacatcgccitgaa
cgaggacctgcgctcttggaccgcggcgacatggcggctcagatcaccagcgcaagtgaggaggcgcccggtgtg
gcggagcagitgagagcctacctggagggcacgtgcgtggagtggtccgcagatacctggagaacgggaaggaga
cgctgcagcgcacgg (SEQ ID NO:244) ;

A*7405 :

15 gctcccactccatgaggtaattcttcacatccgtgtcccgcccgccgaggagccccgcttcatcgccgtggg
ctacgtggacgacacgcagttcgtgcgggttgacagcgacgccgcgagccagaggatggagccgcggcgccgtgg
atagagcaggaggggcccggagtattgggaccaggagacacggaatgtgaaggcccaactcacagGctgaccgagtgg
acctggggaccctgcgcggctactacaaccagagcgaggccggttctcacaccaaccagatgatgtatggctgcga
cgtggggccggacgggcgcctccctccgcggtaccagcaggacgcctacgacggcaaggattacatcgccitgaac
20 gaggacctgcgctcttggaccgcggcgacatggcggctcagatcaccagcgcaagtgaggaggcgcccggtgtgg
cggagcagiltgagagcctacctggagggcacgtgcgtggagtggtccgcagatacctggagaacgggaaggagac
gctgcagcgcacgg (SEQ ID NO:245) ;

A*7406 :

25 gctcccactccatgaggtaattcttcacatccgtgtcccgcccgccgaggagccccgcttcatcgccgtggg
ctacgtggacgacacgcagttcgtgcgggttgacagcgacgccgcgagccagaggatggagccgcggcgccgtgg
atagagcaggaggggcccggagtattgggaccaggagacacggaatgtgaaggcccaactcacagactCaccgagtG
acctggggaccctgcgcggctactacaaccagagcgaggccggttctcacaccaaccagatgatgtatggctgcga

cgtagggccggacgggcgcCtccctccgcggtaccagcaggacgcctacgacggcaaggattacatcgccitgaac
gaggacctgcgcicttggaccgcgcgacatggcggctcagatcaccagcgcaagtagggaggcgggccGtgtgg
cggagcagTtagagccctaccitggagggcacgtgcgtggagtggctccgcagataccitggagaacgggaaggagac
gctgcagcgcacg (SEQ ID NO:246) ;

5 A*7407 :

gctcccactccatgaggtatttcttcacatccgtgtcccgccccggccgcgaggagccccgcttcatcgccgtggg
ctacgtggacgacacgcagttcgtgcggtttgacagcgacgccgagccagaggatggagccgcgggcgccgtgg
atagagcaggagggggccggagtattgggaccaggagacacggaaigtgaaggcccacacagaTtagccgagtG
accitggggacccitgcgcggctactacaaccagagcgaggccggttctcacaccatccagatgatgtatggctgcga

10 cgtagggccggacgggcgcCtccctccgcggtaccagcaggacgcctacgacggcaaggattacatcgccitgaac
gaggacctgcgcicttggaccgcgcgacatggcggctcagatcaccagcgcaagtagggaggcgggccGtgtgg
cggagcagTtagagccctaccitggagggcacgtgcgtggagtggctccgcagataccitggagaacgggaaggagac
gctgcagcgcacgg (SEQ ID NO:247) ;

A*7408 :

15 gctcccactccatgaggtatttcttcacatccgtgtcccgccccggccgcgaggagccccgcttcatcgccgtggg
ctacgtggacgacacgcagttcgtgcggtttgacagcgacgccgagccagaggatggagccgcgggcgccgtgg
atagagcaggagggggccggagtattgggaccaggagacacggaaigtgaaggcccacacagacigaccgagtgg
accitggggacccitgcgcggctactacaaccagagcgaggccggttctcacaccatccagatgatgtatggctgcga
cgtagggccggacgggcgcctccctccgcggtaccagcaggacgcctacgacggcaaggattacatcgccitgaac

20 gaggacctgcgcicttggaccgcgcgacatggcggctcagatcaccagcgcaagtagggaggcgggccAgtagtgg
cggagcagtttagagccctaccitggagggcacgtgcgtggagtggctccgcagataccitggagaacgggaaggagac
gctgcagcgcacgg (SEQ ID NO:248) ;

A*7409 :

25 gctcccactccatgaggtatttcttcacatccgtgtcccGccccggccgcgaggagccccgcttcatcgccgtggg
ctacgtggacgacacgcagttcgtgcggtttgacagcgacgccgagccagaggatggagccgcgggcgccgtgg
atagagcaggagggggccggagtattgggaccaggagacacggaaigtgaaggcccacacagacigaccgagtgg
accitggggacccitgcgcggctactacaaccagagcgaggccggttctcacaccatccagatgatgtatggctgcga

cgiggggccggacggggccctccgccgggtaccagcaggacgcttacgacggcaaggattacatcgccctgaac
gaggacctgcgctcttgaccgcggcgacatggcggctcagatcacccagcgaagtgggaggcgcccgctgg
cggagcagttgagagcctacciggagggcacgtgcgtggagtggctccgcagatacciggagaacgggaaggagac
gctgcagcgcacgg(SEQ ID NO:249) ;

5 A*8001 :

Atggccgtcatgccgccccgaaccctccctctgctactctcgggggccctggccctgaccagacctgggcaggct
cccaticcatgaggtatitcttcacatccgtgtcccgcccgccggggagccccgcttcatcgagttgggcta
cgiggacgactcgagttcgtgcagttcgacagcgacgccgcgagccagaggatggagccgcccggcgccgtggata
gagcaggaggagccggagtattgggacgaggagacacggaatgigaaggccactcacagactaaccgagcgaacc
10 tggggacccctgcgcggctactacaaccagagcgaggacggttctcacaccatccagataatgtatggctgcgacgt
ggggtcggacgggcgttccgccgggtaccggcaggacgcttacgacggcaaggattacatcgccctgaacgag
gacctgcgctcttgaccgcggcgacatggcggctcagatcaccaagcgaagtgggaggcgcccgctcgggcgg
agcagctgagagcctacciggaggcgagtgcgtggacgggtccgcagatacciggagaacgggaaggagacgt
gcagcgacggaccccccaagacacatacgaccaccaccccatctctgaccaatgaggccactctgaggctcgtgg
15 gcccctgagcttctacccctgcggagatcacactgacctggcagcgggatggggaggaccagaccaggacacggagc
tcgtggagaccaggccctgcaggggatggaaccttcagaagtggcgccgtgtggtggtaacctctggaaaggagaa
gagatacacctgccatgtgcagcatgagggtctgcccGagccctcaccttgagatgggag
(SEQ ID NO:25) ;

20

The probe list A1 is shown in Tables 1-1 to 1-7
and the probe list A2 is shown in Tables 2-1 to 2-6.
The allele-probe lists are shown in Tables 3-1 to 3-9
and Tables 4-1 to 4-9.

25

Table 1-1

Probe No.	Base Sequence
0	g ccc cgc ttc atc gcC (SEQ ID No: 2 5 1)
1	gac cag gag aca cgg aat A (SEQ ID No: 2 5 2)
2	gcg gag cag cgg aga gT (SEQ ID No: 2 5 3)
3	a gtc tac ctg gag ggc C (SEQ ID No: 2 5 4)
4	gtc tac ctg gag ggc cG (SEQ ID No: 2 5 5)
5	agg tgc tgg gcc ctg G (SEQ ID No: 2 5 6)
6	g gtg gtg cct tct gga G (SEQ ID No: 2 5 7)
7	c acc ctg aga tgg gag cT (SEQ ID No: 2 5 8)
8	cc ctg aga tgg gag ctG (SEQ ID No: 2 5 9)
9	g gac atg gca gct cag atT (SEQ ID No: 2 6 0)
10	cac tcc atg agg tat ttc tC (SEQ ID No: 2 6 1)
11	c cgg ccc ggc agt ggA (SEQ ID No: 2 6 2)
12	t tct cac acc atc cag atG (SEQ ID No: 2 6 3)
13	c cat gcg gcg gag cag T (SEQ ID No: 2 6 4)
14	cat gcg gcg gag cag tT (SEQ ID No: 2 6 5)
15	ata gag cag gag agg ccT (SEQ ID No: 2 6 6)
16	c tca cag act gac cga gA (SEQ ID No: 2 6 7)
17	c tac aac cag agc gag gC (SEQ ID No: 2 6 8)
18	ga gtc tac ctg gag ggc T (SEQ ID No: 2 6 9)
19	gtg gac gac acg cag tta (SEQ ID No: 2 7 0)
20	tg cta ctc tgg ggg gcT (SEQ ID No: 2 7 1)
21	g gcc cac tca cag act C (SEQ ID No: 2 7 2)
22	g gcc ggt tct cac acc G (SEQ ID No: 2 7 3)
23	t tct cac acc gtc cag aG (SEQ ID No: 2 7 4)
24	c gac gtg ggg tgg gac T (SEQ ID No: 2 7 5)
25	gg gag gcg gcc cat gT (SEQ ID No: 2 7 6)
26	c cat gtg gcg gag cag tT (SEQ ID No: 2 7 7)
27	gcc tac ctg gag ggc aC (SEQ ID No: 2 7 8)
28	ga gct gtg gtc gct gcT (SEQ ID No: 2 7 9)
29	ag ccc cgc ttc atc gcA (SEQ ID No: 2 8 0)
30	ccg gag tat tgg gac gG (SEQ ID No: 2 8 1)

Table 1-2

Probe No.	Base Sequence
31	ggc ttg cat tcc ctc cG (SEQ ID No :32)
32	c cca gtt ggg acg agt gT (SEQ ID No :33)
33	ct gct gct gct gct gcT (SEQ ID No :34)
34	a gaa gat gtc ctg gga aaC (SEQ ID No :35)
35	t gtg cag tca ggg ttt ctT (SEQ ID No :36)
36	gcc tca gag ggc aac atC (SEQ ID No :37)
37	ct gct gct gct gct gcT (SEQ ID No :38)
38	ttc tat ccc cgg aat atc aT (SEQ ID No :39)
39	gtt gct gct gct gct gcT (SEQ ID No :40)
40	cag acc ttg gcc atg aac A (SEQ ID No :41)
41	gg aat cac agc act cac G (SEQ ID No :42)
42	a cgg cga tat cta aaa tcc A (SEQ ID No :43)
43	ctc tcc caa aac ctg gag T (SEQ ID No :44)
44	ttc ttg aag gaa gat gcc G (SEQ ID No :45)
45	cat gaa gac aac agc acc aA (SEQ ID No :46)
46	ggg ttt ctc gct gag gG (SEQ ID No :47)
47	caa gga gag gag cag agT (SEQ ID No :48)
48	g gcc acc agg att tgc G (SEQ ID No :49)
49	c agg gct tct ggc ttc tG (SEQ ID No :50)
50	ag aaa aca tca gct gca gaT (SEQ ID No :51)
51	at caa cac cca gtt ggg aT (SEQ ID No :52)

Table 1-3

Probe No.	Base Sequence
61	ca cag act cac cga gtg G (SEQ ID No: 3 1 2)
62	c gcg gcg gac atg gcG (SEQ ID No: 3 1 3)
63	gt ccg gag tat tgg gac G (SEQ ID No: 3 1 4)
64	ac ggg gag aca cgg aaC (SEQ ID No: 3 1 5)
65	ca gtg ggc tac gtg gac A (SEQ ID No: 3 1 6)
66	tgg gag acg gcc cat gT (SEQ ID No: 3 1 7)
67	c cat gag gcg gag cag tT (SEQ ID No: 3 1 8)
68	a gct cag acc acc aag cA (SEQ ID No: 3 1 9)
69	cat gcg gcg gag cag cA (SEQ ID No: 3 2 0)
70	cg tgg ata gag cag gag A (SEQ ID No: 3 2 1)
71	gac ggg gag aca cgg C (SEQ ID No: 3 2 2)
72	c tgg gcg ggc tct caG (SEQ ID No: 3 2 3)
73	tc gac agc gac gcc gG (SEQ ID No: 3 2 4)
74	c acc gtc cag agg atg tC (SEQ ID No: 3 2 5)
75	cgg aaa gtg aag gcc caG (SEQ ID No: 3 2 6)
76	g gcc cag tca cag act C (SEQ ID No: 3 2 7)
77	g gct cag atc acc aag cA (SEQ ID No: 3 2 8)
78	gcg gag cag ttg aga gC (SEQ ID No: 3 2 9)
79	g ggc acg tgc gtg gaG (SEQ ID No: 3 3 0)
80	g tgg gag gcg gcc cG (SEQ ID No: 3 3 1)
81	gg gag gcg gcc cgt gT (SEQ ID No: 3 3 2)
82	c cgc ggg tac cag cag T (SEQ ID No: 3 3 3)
83	g gag ccc cgc ttc atc T (SEQ ID No: 3 3 4)
84	gac cag gag aca cgg aaA (SEQ ID No: 3 3 5)
85	at tgg gac gag gag aca G (SEQ ID No: 3 3 6)
86	gac gag gag aca ggg aaA (SEQ ID No: 3 3 7)
87	g aag gcc cac tca cag aG (SEQ ID No: 3 3 8)
88	g agg taf ttc ttc aca tcc A (SEQ ID No: 3 3 9)
89	ttc ctc cgc ggg tat gaA (SEQ ID No: 3 4 0)
90	gag tat tgg gac cgg aaC (SEQ ID No: 3 4 1)

Table 1-4

Probe No.	Base Sequence
91	cgg aat gtg aag gcc caG (SEQ ID No: 3 4 2)
92	g gcc ggt tct cac acc C (SEQ ID No: 3 4 3)
93	t tct cac acc ctc cag aG (SEQ ID No: 3 4 4)
94	c cgg ccc ggc cgc gA (SEQ ID No: 3 4 5)
95	cgc ggg tac cac cag tT (SEQ ID No: 3 4 6)
96	ca cag act gac cga gtg G (SEQ ID No: 3 4 7)
97	g ttg aga gcc tac ctg gaT (SEQ ID No: 3 4 8)
98	cat gag gcg gag cag cT (SEQ ID No: 3 4 9)
99	ctg aga gcc tac ctg gaT (SEQ ID No: 3 5 0)
100	tgg ata gag cag gag ggT (SEQ ID No: 3 5 1)
101	cag aga gcc tac ctg gaT (SEQ ID No: 3 5 2)
102	ggc ctg gtt ctc ctt gC (SEQ ID No: 3 5 3)
103	g aga gcc tac ctg gat gC (SEQ ID No: 3 5 4)
104	ggc tgc gac gtg ggg T (SEQ ID No: 3 5 5)
105	g ggc cgg tgc gtg gaG (SEQ ID No: 3 5 6)
106	ggc cgg tgc gtg gag T (SEQ ID No: 3 5 7)
107	gc tct tgg acc gcg gCA (SEQ ID No: 3 5 8)
108	gg ccc ggc cgc ggg A (SEQ ID No: 3 5 9)
109	gg gag gcg gcc cgt gA (SEQ ID No: 3 6 0)
110	cgt gag gcg gag cag cA (SEQ ID No: 3 6 1)
111	g gca gct cag atc acc G (SEQ ID No: 3 6 2)
112	g ccg gac ggg cgc ttA (SEQ ID No: 3 6 3)
113	g cag aga gcc tac ctg C (SEQ ID No: 3 6 4)
114	g ccg gag tat tgg gac cT (SEQ ID No: 3 6 5)
115	g gca gct cag atc acc aG (SEQ ID No: 3 6 6)
116	g gag gcg gcc cgt cG (SEQ ID No: 3 6 7)
117	ac gag gag aca ggg aaa G (SEQ ID No: 3 6 8)
118	cc cag ccc acc gtc cA (SEQ ID No: 3 6 9)
119	c cgt gtg gcg gag cag T (SEQ ID No: 3 7 0)
120	gcg gag cag tgg aga gC (SEQ ID No: 3 7 1)

Table 1-5

Probe No.	Base Sequence
121	ggc aag gat tac atc gcc T (SEQ ID No: 372)
122	cgt gtg gcg gag cag tT (SEQ ID No: 373)
123	c tcc cac tcc atg agg tG (SEQ ID No: 374)
124	cg ctc cgc tac tac aac G (SEQ ID No: 375)
125	ctg cgg atc gcg ctc C (SEQ ID No: 376)
126	gcg gag cag cag aga gC (SEQ ID No: 377)
127	a tct tcc cag ccc acc G (SEQ ID No: 378)
128	ctg ggc ttc tac cct gcA (SEQ ID No: 379)
129	cgc ggg tac cac cag taT (SEQ ID No: 380)
130	ag acg ctg cag cgc acT (SEQ ID No: 381)
131	g gcg gct cag atc acc C (SEQ ID No: 382)
132	ggg aaa gtg aag gcc caG (SEQ ID No: 383)
133	cc tgg gca ggc tcc caA (SEQ ID No: 384)
134	g ggc acg tgc gtg gac T (SEQ ID No: 385)
135	gac ggg cgc ttc ctc cA (SEQ ID No: 386)
136	gg acc gcg gcg gac aG (SEQ ID No: 387)
137	cg gag tat tgg gac gag C (SEQ ID No: 388)
138	a cag act gac cga gag aG (SEQ ID No: 389)
139	c cag agg atg gag ccg T (SEQ ID No: 390)
140	g agc cag agg atg gag cT (SEQ ID No: 391)
141	gc tcc cac tcc atg agC (SEQ ID No: 392)
142	g cct gca ggg gat ggG (SEQ ID No: 393)
143	c cag cgc aag tgg gag A (SEQ ID No: 394)
144	c cgc ggg tac cag cag A (SEQ ID No: 395)
145	gcc tac ctg gag ggc cT (SEQ ID No: 396)
146	tc cgc ggg tac cag cG (SEQ ID No: 397)
147	ttc ctc cgc ggg tac cA (SEQ ID No: 398)
148	gg tac cag cag gac gcT (SEQ ID No: 399)
149	cg cag ttc gtg cgg ttG (SEQ ID No: 400)
150	c cag agc gag gac ggt A (SEQ ID No: 401)

Table 1-6

Probe No.	Base Sequence
151	cag atg atg tat ggc tgc C (SEQ ID No: 4 0 2)
152	g atg gag ccg cgg gca (SEQ ID No: 4 0 3)
153	g.gac ctg cag aca cgg C (SEQ ID No: 4 0 4)
154	gag acg ctg cag cgc G (SEQ ID No: 4 0 5)
155	tgg gag gcg gcc cgt T (SEQ ID No: 4 0 6)
156	gg gag gcg gcc cgt C (SEQ ID No: 4 0 7)
157	g ggc tac gtg gac gac G (SEQ ID No: 4 0 8)
158	cac acc atc cag ata atg C (SEQ ID No: 4 0 9)
159	gtg cag cat gag ggt ctC (SEQ ID No: 4 1 0)
160	gg tac cgg cag gac gcT (SEQ ID No: 4 1 1)
161	c cac tcc atg agg tat ttc A (SEQ ID No: 4 1 2)
162	g aca cgg aat gtg aag gG (SEQ ID No: 4 1 3)
163	c cta gtt ctc itt gga gct A (SEQ ID No: 4 1 4)
164	gg ccg gac ggg cgc C (SEQ ID No: 4 1 5)
165	gcc tac ctg gat ggc aC (SEQ ID No: 4 1 6)
166	t ggc acg tgc gtg gag T (SEQ ID No: 4 1 7)
167	gac cag gag aca ggg aaA (SEQ ID No: 4 1 8)
168	gc acg gac ccc ccc aG (SEQ ID No: 4 1 9)
169	ac gag gac ctg agt tcC (SEQ ID No: 4 2 0)
170	gcg ccg tgg ata gag cG (SEQ ID No: 4 2 1)
171	g cgg gcg ccg tgg atG (SEQ ID No: 4 2 2)
172	c ccc atc gtg ggc atc C (SEQ ID No: 4 2 3)
173	ctg cag cgc acg gac G (SEQ ID No: 4 2 4)
174	g gac gcc ccc aag acG (SEQ ID No: 4 2 5)
175	ctc ttt gga gct gtg atc G (SEQ ID No: 4 2 6)
176	gac ggc aag gat tac atc T (SEQ ID No: 4 2 7)
177	gtc tac ctg gag ggc aC (SEQ ID No: 4 2 8)
178	cgg aga gcc tac ctg gaT (SEQ ID No: 4 2 9)
179	g gac ggt tct cac acc C (SEQ ID No: 4 3 0)
180	g ggc gag tgc gtg gag T (SEQ ID No: 4 3 1)

Table 1-7

Probe No.	Base Sequence
181	g gag tgg ctc cgc aga C (SEQ ID No.:4 3 2)
182	ga acc ttc cag aag tgg gT (SEQ ID No.:4 3 3)
183	cc atg agg tat ttc tac acT (SEQ ID No.:4 3 4)
184	g agg tat ttc tac acc tcc A (SEQ ID No.:4 3 5)
185	cgc ggg tac cgg cag C (SEQ ID No.:4 3 6)
186	cat gtg gcg gag cag cT (SEQ ID No.:4 3 7)
187	g ccg gag tat tgg gac G (SEQ ID No.:4 3 8)
188	ag tgg gag gcg gcc cT (SEQ ID No.:4 3 9)
189	gc ggg tac cgg cag gT (SEQ ID No.:4 4 0)
190	tgg aga gcc tac ctg gaT (SEQ ID No.:4 4 1)
191	tg ggg tcg gac ggg cA (SEQ ID No.:4 4 2)
192	gc aga tac ctg gag aac C (SEQ ID No.:4 4 3)
193	gac ctg ggg acc ctg cA (SEQ ID No.:4 4 4)
194	gt tct cac acc atc cag aG (SEQ ID No.:4 4 5)
195	g gcc ctg acc cag acc A (SEQ ID No.:4 4 6)
196	c ctc ctc ctg cta ctc tT (SEQ ID No.:4 4 7)
197	ctc ctc cgc ggg tac cA (SEQ ID No.:4 4 8)
198	gac cga gtg gac ctg gC (SEQ ID No.:4 4 9)
199	g aag gcc cac tca cag G (SEQ ID No.:4 5 0)
200	ca cag att gac cga gtg G (SEQ ID No.:4 5 1)
201	c aag tgg gag gcg gcc A (SEQ ID No.:4 5 2)
202	c ttc aca tcc gtg tcc cC (SEQ ID No.:4 5 3)
203	cag ccc acc atc ccc atT (SEQ ID No.:4 5 4)

Table 2-1

Probe No.	Base Sequence
0	a gag acc agA gac ttg aca (SEQ ID No:53)
1	ctg gag act Aag gaa tgg a (SEQ ID No:54)
2	cga tat cta Aaa tcc ggc g (SEQ ID No:55)
3	cta aaa tcc Ggc gta gtc c (SEQ ID No:56)
4	c aca ctg aGc tgg cgt c (SEQ ID No:57)
5	att att ttc taC gtc tgt tgt t (SEQ ID No:58)
6	tg ctg tcc Ggg gat gga (SEQ ID No:59)
7	acc cgc agI gag gcc tc (SEQ ID No:60)
8	g agg aga aGa gtg ccc c (SEQ ID No:61)
9	tg atg tca gCt ctt ggg tc (SEQ ID No:62)
10	c ctg cgc tAt gac agg c (SEQ ID No:63)
11	gaa tgg aca Gtg ccc cag (SEQ ID No:64)
12	c aca ctg aCc tgg cgt c (SEQ ID No:65)
13	gg att tgc cGa gga gag g (SEQ ID No:66)
14	gaa tcc agc Ata gtc ctg a (SEQ ID No:67)
15	a gag acc agG gac ttg ac (SEQ ID No:68)
16	ctg gag act GAg gaa tgg (SEQ ID No:69)
17	gtt gct gct G gct gct g (SEQ ID No:70)
18	g gtg gcc acI agg att tg (SEQ ID No:71)
19	gct gct g gct gct gcI a (SEQ ID No:72)
20	agc gag gcA tca gag gg (SEQ ID No:73)
21	tcc caa aac Gtg gag act g (SEQ ID No:74)
22	at ttc tac taI gat ggg gag (SEQ ID No:75)
23	cta gaa tcc Agc gta gtc c (SEQ ID No:76)
24	t ggg tcc Gct ggc tcc (SEQ ID No:77)
25	cc aag aca cIc tat cac gc (SEQ ID No:78)
26	a gag gag caA agg ttc acc (SEQ ID No:79)
27	cga tat cta Gaa tcc ggc g (SEQ ID No:80)
28	tac tac gat Agg gag ctc t (SEQ ID No:81)
29	g ggt cca gGg ctc gtg (SEQ ID No:82)
30	cag gat ggg Cta tct ttg a (SEQ ID No:83)

Table 2-2

Probe No.	Base Sequence
31	at tcc ctc cGg gag att ag (SEQ ID No: 84)
32	t gct gct gct gct gcT at (SEQ ID No: 85)
33	ct gct gct gcT att ttt gtt (SEQ ID No: 86)
34	c ctg gga aaC aag aca tgg (SEQ ID No: 87)
35	a ggg ttt ctT gct gag gta (SEQ ID No: 88)
36	g ggc aac atC acc gtg ac (SEQ ID No: 89)
37	gct gct gct gct gcT att (SEQ ID No: 90)
38	cgg aat atc aTc ctg acc tg (SEQ ID No: 91)
39	gcc atg aac Atc agg aat tt (SEQ ID No: 92)
40	gc act cac Gct gtg ccc (SEQ ID No: 93)
41	cta aaa tcc Agc gta gtc c (SEQ ID No: 94)
42	aac ctg gag Tct gag gaa t (SEQ ID No: 95)
43	gaa gat gcc Gtg aag acc (SEQ ID No: 96)
44	c agc acc aAg agc tcc c (SEQ ID No: 97)
45	c gct gag gGa cat ctg g (SEQ ID No: 98)
46	g gag cag agT ttc acc tg (SEQ ID No: 99)
47	agg att tgc Gaa gga gag g (SEQ ID No: 100)
48	ct ggc ttc tGt ccc tgg a (SEQ ID No: 101)
49	a gct gca gaT ggt cca ga (SEQ ID No: 102)
50	ca gtt ggg aTg agt gac c (SEQ ID No: 103)

Table 2-3

Probe No.

Base Sequence

61	g aca cgg aaC gtg aag gc (SEQ ID No : 5 1 6)
62	tac gtg gac Aac acg cag (SEQ ID No : 5 1 7)
63	cc acc aag cAc aag tgg g (SEQ ID No : 5 1 8)
64	ag cag gag Agt ccg gag (SEQ ID No : 5 1 9)
65	gag aca cgg Caa gtg aag (SEQ ID No : 5 2 0)
66	g ggc tct caG tcc atg ag (SEQ ID No : 5 2 1)
67	c gac gcc gGg agc cag (SEQ ID No : 5 2 2)
68	g agg atg tCt ggc tgc g (SEQ ID No : 5 2 3)
69	g aag gcc caG tca cag ac (SEQ ID No : 5 2 4)
70	tc acc aag cAc aag tgg g (SEQ ID No : 5 2 5)
71	ag ttg aga gCc tac ctg g (SEQ ID No : 5 2 6)
72	tgc gtg gaG tgg ctc cg (SEQ ID No : 5 2 7)
73	gcg gcc cGt gtg gcg (SEQ ID No : 5 2 8)
74	g gcc cgt gTg gcg gag (SEQ ID No : 5 2 9)
75	tac cag cag Tac gcc tac (SEQ ID No : 5 3 0)
76	cgc ttc atc Tca gtg ggc (SEQ ID No : 5 3 1)
77	gag gag aca Ggg aaa gtg (SEQ ID No : 5 3 2)
78	g aca ggg aaA gtg aag gc (SEQ ID No : 5 3 3)
79	ac tca cag aGt cac cga g (SEQ ID No : 5 3 4)
80	ttc aca tcc Atg tcc cgg (SEQ ID No : 5 3 5)
81	c ggg tat gaA cag cac gc (SEQ ID No : 5 3 6)
82	g gac cgg aaC aca cgg aa (SEQ ID No : 5 3 7)
83	tct cac acc Ctc cag atg (SEQ ID No : 5 3 8)
84	ct cac acc Ctc cag agg (SEQ ID No : 5 3 9)
85	cc ctc cag aGg atg tat g (SEQ ID No : 5 4 0)
86	ggc cgc gAg gag ccc (SEQ ID No : 5 4 1)
87	c cac cag tTc gcc tac g (SEQ ID No : 5 4 2)
88	c tac ctg gaT ggc acg tg (SEQ ID No : 5 4 3)
89	g gag cag cTg aga gcc t (SEQ ID No : 5 4 4)
90	cag gag ggT ccg gag ta (SEQ ID No : 5 4 5)

Table 2-4

Probe No.	Base Sequence
91	ctg gag aac Cgg aag gag (SEQ ID No : 5 4 6)
92	c ctg gat gCc acg tgc g (SEQ ID No : 5 4 7)
93	c gtg ggg Tcg gac ggg (SEQ ID No : 5 4 8)
94	acc gcg gcA gac atg gc (SEQ ID No : 5 4 9)
95	c cgc ggg Aag ccc cg (SEQ ID No : 5 5 0)
96	gcg gcc cGt gag gcg (SEQ ID No : 5 5 1)
97	g gcc cgt gAg gcg gag (SEQ ID No : 5 5 2)
98	cag atc acc Gag cgc aag (SEQ ID No : 5 5 3)
99	ggg cgc tTA ctc cgc g (SEQ ID No : 5 5 4)
100	c tac ctg Cag ggc cgg (SEQ ID No : 5 5 5)
101	at tgg gac cTg cag aca c (SEQ ID No : 5 5 6)
102	ag atc acc aGg cgc aag t (SEQ ID No : 5 5 7)
103	gcc cgt cGg gcg gag (SEQ ID No : 5 5 8)
104	aca ggg aaa Gtg aag gcc (SEQ ID No : 5 5 9)
105	g aag tgg gcA gct gtg gt (SEQ ID No : 5 6 0)
106	g tgg aga gCc tac ctg g (SEQ ID No : 5 6 1)
107	tac atc gcc Ttg aac gag g (SEQ ID No : 5 6 2)
108	cc atg agg tGt ttc tcc ac (SEQ ID No : 5 6 3)
109	tac tac aac Gag agc gag g (SEQ ID No : 5 6 4)
110	tc gcg ctc Cgc tac tac (SEQ ID No : 5 6 5)
111	g cag aga gCc tac ctg g (SEQ ID No : 5 6 6)
112	c tac cct gcA gag atc ac (SEQ ID No : 5 6 7)
113	c cac cag taT gcc tac ga (SEQ ID No : 5 6 8)
114	cag atc acc Cag cgc aag (SEQ ID No : 5 6 9)
115	a ggc tcc caA tcc atg ag (SEQ ID No : 5 7 0)
116	t gtg gtg gTA cct tct gg (SEQ ID No : 5 7 1)
117	cg gag cag Tgg aga gtc (SEQ ID No : 5 7 2)
118	c gtg gac Tgg ctc cgc (SEQ ID No : 5 7 3)
119	c ttc ctc cAc ggg tac c (SEQ ID No : 5 7 4)
120	g gcg gac aGg gcg gct (SEQ ID No : 5 7 5)

Table 2-5

Probe No.	Base Sequence
121	tca cag act Cac cga gag (SEQ ID No : 576)
122	gg gac gag Cag aca ggg (SEQ ID No : 577)
123	c cga gag aGc ctg cgg (SEQ ID No : 578)
124	ac tca cag aTt gac cga ga (SEQ ID No : 579)
125	g gag ccg Tgg gcg cc (SEQ ID No : 580)
126	g atg gag cTg cgg gcg (SEQ ID No : 581)
127	c tcc atg agC tat ttc tcc (SEQ ID No : 582)
128	ggg gat ggG acc ttc ca (SEQ ID No : 583)
129	cct tct gga Cag gag cag (SEQ ID No : 584)
130	tac cag cag Aac gct tac g (SEQ ID No : 585)
131	g gag ggc cTg tgc gtg (SEQ ID No : 586)
132	g tac cag cGg gac gct t (SEQ ID No : 587)
133	c ggg tac cAg cag gac g (SEQ ID No : 588)
134	cag gac gcT tac gac gg (SEQ ID No : 589)
135	gtg cgg ttG gac agc ga (SEQ ID No : 590)
136	gag gac ggt Act cac acc (SEQ ID No : 591)
137	t ggc tgc Cac gtg ggg (SEQ ID No : 592)
138	ccg cgg gcA ccg tgg (SEQ ID No : 593)
139	cag aca cgg Cat gtg aag (SEQ ID No : 594)
140	g gcc cgt Tgg gcg gag (SEQ ID No : 595)
141	g gcc cgt Cgg gcg ga (SEQ ID No : 596)
142	tg gac gac Gcg cag ttc (SEQ ID No : 597)
143	cag ata atg Cat ggc tgc g (SEQ ID No : 598)
144	gag ggt ctC ccc aag cc (SEQ ID No : 599)
145	agg tat ttc Acc aca tcc g (SEQ ID No : 600)
146	at gtg aag gGc cac tca c (SEQ ID No : 601)
147	c acg gag ctT gtg gag ac (SEQ ID No : 602)
148	c ggg cgc Ctc ctc cg (SEQ ID No : 603)
149	g gat ggc aCg tgc gtg g (SEQ ID No : 604)
150	c ccc ccc aGg acg cat (SEQ ID No : 605)

Table 2-6

Probe No.	Base Sequence
151	ctg agc tcC tgg acc gc (SEQ ID No : 606)
152	g ata gag cGg gag ggg c (SEQ ID No : 607)
153	ccg tgg atG gag cag ga (SEQ ID No : 608)
154	c acg gac Gcc ccc aag (SEQ ID No : 609)
155	ag tgg gcg Tct gtg gtg (SEQ ID No : 610)
156	c ccc aag acG cat atg ac (SEQ ID No : 611)
157	g cag gag Agg ccg gag (SEQ ID No : 612)
158	gat tac atc Tcc ctg aac g (SEQ ID No : 613)
159	tc cgc aga Cac ctg gag (SEQ ID No : 614)
160	g aag tgg gTg gct gtg g (SEQ ID No : 615)
161	t ttc tac acT tcc gtg tcc (SEQ ID No : 616)
162	ac acc tcc Atg tcc cgg (SEQ ID No : 617)
163	c cgg cag Cac gcc tac (SEQ ID No : 618)
164	tat tgg gac Gag gag aca c (SEQ ID No : 619)
165	g gcg gcc cTt gtg gcg (SEQ ID No : 620)
166	c cgg cag gTc gcc tac (SEQ ID No : 621)
167	g gac ggg cAc ttc ctc c (SEQ ID No : 622)
168	g acc ctg cAc ggc tac t (SEQ ID No : 623)
169	cc atc cag aGg atg tat gg (SEQ ID No : 624)
170	c cag acc Agg gcg ggc (SEQ ID No : 625)
171	g cta ctc tTg ggg gcc c (SEQ ID No : 626)
172	g gac ctg gCg acc ctg (SEQ ID No : 627)
173	cac tca cag Gct gac cga (SEQ ID No : 628)
174	g gcg gcc Agt gtg gcg (SEQ ID No : 629)
175	gtg tcc cCg ccc ggc (SEQ ID No : 630)
176	t ctg ccc Gag ccc ctc (SEQ ID No : 631)

Table 3-1

Allele Number	Probe Number for Detection									
A*010101	0	1	2	3	4	5	6	7	8	
A*010102	9									
A*0102	10	11								
A*0103	12									
A*0106	13	14								
A*0107	15	16	17							
A*0108	18									
A*0109	19									
A*020101	20	21	22	23	24	25	26	27	28	
A*020102	29	30	31	21	22	23	24	32	33	34
A*020103	37									
A*020104	38									
A*020105	39									
A*020106	40									
A*020107	41	42								
A*020108	43									
A*020109	31	21	22	23	24	25	44	26	27	42
A*0202	45	42								
A*0203	20	46	47	48	27	28				
A*0204	20	21	22	24	25	26	27	28		
A*0205	45	28								
A*0206	20	49	21	22	23	24	25	26	27	28
A*0207	50									
A*0208	49	45								
A*0209	51									
A*0210	20	23	52	25	26	27	28			
A*0211	53	42	28							

Allele Number	Probe Number for Detection															
A*0212	20		25		54		27		28							
A*0213	20		55		56		27		28							
A*0214	45		26		28											
A*0216	57		42		28											
A*021701	20		58		24		25		26		27		28			
A*021702	20		58		24		25		26		27		59			
A*0218	60															
A*0219	61		22		62		25		54		27					
A*022001	29	63	30	21	22	23	24	32	33	34	35	25	26	27	36	
A*022002	64															
A*0221	65															
A*0222	20		21		22		23		24		25		44		27	28
A*0224	29	30	31	21	22	23	24	32	33	35	25	26	27	36		
A*0225	46		66		26		27									
A*0226	20		55		67		27		28							
A*0227	22		68		69		27		36							
A*0228	70		68		25		26		36							
A*0229	71		68													
A*0230	72															
A*0231	73															
A*0233	74															
A*0234	31	75	76	22	23	24	25	44	26	27	42					
A*0235	31	75	22	23	24	32	33	34	35	25	26	27	36			
A*0236	29	30	31	21	22	23	24	32	33	34	35	25	26	27		
A*0237	22		68		25		54		27							

[illegible]

Table 3-4

Allele Number	Probe Number for Detection							
A*0308	96	55	48	67	97			
A*0309	76	61	55	48	67	97		
A*0310	96	104	62	25	54	27	79	36
A*110101	49	91	96	69	105	106		
A*110102	107							
A*1102	108							
A*1103	80	109	110					
A*1104	49	91	96	69	27	79	36	
A*1105	111							
A*1106	91	76	61	69	105	106		
A*1107	112							
A*1108	49	91	96	55				
A*1109	113							
A*1110	49	90	96	69	106			
A*1111	114	96	69	106				
A*1112	49	91	96	17	69	105	106	
A*1113	115							
A*1114	108	116						
A*2301	117	118						
A*2302	85	34	80	81	119	120	27	
A*2303	33	121	80	122				
A*2304	85	34	80	81	122	78	27	79 36
A*2305	123	122						
A*2306	124							
A*2309	118							
A*240201	85	125	54	126	127			
A*240202	85	125	17	58	104	33	34	54 126 27
A*240203	128							
A*240204	129							

Table 3-5

Allele Number	Probe Number for Detection									
A*240301	126	36	127							
A*240302	130									
A*2404	85	54	126	127						
A*2405	85	131	54	126	27					
A*2406	85	34	62	25	44	120	27			
A*2407	132	125	54	126	127					
A*2408	133	28								
A*2410	85	54	126	105	106					
A*2413	85	34	62	25	26	78	27			
A*2414	85	24	33	34	62	54	126	27		
A*2415	85	125	17	92	33	34	62	54	126	27
A*2417	85	125	17	58	104	34	62	54	126	27
A*2418	34	55	48	67	97					
A*2419	85	132	96	58	104	33	34	62	54	126 27
A*2420	85	125	17	58	104	33	34	62	54	126 27
A*2421	85	125	17	58	104	33	62	54	126	27
A*2422	44	36	127							
A*2423	85	54	126	27	134					
A*2424	91	58	34	80	81	122	78	27		
A*2425	123	54								
A*2426	135									
A*2427	136									
A*2428	85	61	17	58	104	33	34	62	54	126 27
A*2429	125	17	58	33	34	62	54	126	27	
A*2430	85	21	125	17	58	104	33	34	62	54 126 27
A*2431	137	25	54	27						
A*2432	138	34	54	27						
A*2433	62	25	54	27	42					
A*2434	53	54								

Table 3-6

Allele Number		Probe Number for Detection						
A*2435	139							
A*2437	140							
A*2438	141							
A*2501	138	142	28					
A*2502	91	138	142	28				
A*2503	138	143	47	48	106			
A*2504	138	47	56	106				
A*2601	90	48	142					
A*2602	144							
A*2603	21	61	48	142				
A*2604	145							
A*2605	16	48	142					
A*2606	146							
A*2607	31	48	142					
A*2608	56	142						
A*2609	147	131	143	47	27			
A*2610	34	131	143	47	48			
A*2612	131	143	66	44				
A*2613	91	147	131	143	47	48		
A*2614	49	90	147	148	55	48		
A*2615	149							
A*2616	10	90	147	131	143	47	48	
A*2617	150							
A*2618	147	148	80	81	119			
A*29010101	151							
A*2902	152	36	28					
A*2903	152	28						
A*2904	153	80						
A*2905	152	56	36					

Table 3-7

Allele Number	Probe Number for Detection							
A*2906	122	154						
A*2907	152	58	122	36				
A*3001	10	15	155					
A*3002	11	15	156	27	36			
A*3003	11	156	27	36				
A*3004	11	25	36					
A*3006	157							
A*3007	86	156	27	36				
A*3008	49	15	155					
A*3009	11	81	122	36				
A*3010	158							
A*3011	10	155						
A*3012	15	156	27	36				
A*310102	15	121	159					
A*3102	84	53	104	147	121	80	122	36
A*3103	53	160	80	122	36			
A*3104	160	159						
A*3105	15	53	104	147	121	80	122	
A*3106	15	53	104	121	80	122	36	
A*3107	15	125	147	121	81	122	36	
A*3108	161	85	125	147	121	122	36	
A*3109	162							
A*3201	125	122	163					
A*3202	54	163						
A*3203	125	164	80	122				
A*3204	138	97	165	166				
A*3205	167	125	122	163				
A*3206	138	25	26	27	36			
A*3207	10	138	80	81	122	27	36	

Table 3-8

Allele Number		Probe Number for Detection							
A*3301	168								
A*3303	90	121	159						
A*3304	169								
A*3305	170								
A*3306	171								
A*3401	172								
A*3402	47	67	27	36	173	174	175	28	
A*3403	160	55	67	27					
A*3404	70	47	67	36					
A*3405	176								
A*3601	177	79							
A*3602	178								
A*3603	179	177	79	36					
A*3604	105								
A*4301	114	142	28						
A*6601	91	96	48	142					
A*6602	57	175	28						
A*6603	47	57	180						
A*6604	47	181							
A*680101	49	91	104	44	182	28			
A*680102	183	91	104	44	182	28			
A*6802	184	28							
A*680301	183	104	44	182	28				
A*680302	183	35	44						
A*6804	90	53	68	36					
A*6805	183	21	35	44					
A*6806	91	89	68	25					
A*6807	91	185	68	25					

Table 4-1

Allele Number	Probe Number for Detection														
A*010101	0	1	2	3	4	5	6	7							
A*010102	8														
A*0102	9	10													
A*0103	11														
A*0106	12	13													
A*0107	14	15	16												
A*0108	17														
A*0109	18														
A*020101	19	20	21	22	23	24	25	13	26	27					
A*020102	28	29	20	21	22	23	24	30	31	32	33	25	13	26	34
A*020103	35														
A*020104	36														
A*020105	37														
A*020106	38														
A*020107	39	27													
A*020108	40														
A*020109	20	21	22	23	24	25	12	13	26	27					
A*0202	41	27													
A*0203	19	42		43		44	26	27							
A*0204	19	20	21		45	24	25	13	26	27					
A*0205	46	41	27												
A*0206	19	46	20	21	22	23	24	25	13	26	27				
A*0207	47														
A*0208	46	41													
A*0209	48														
A*0210	19	49		50		25	13	26	27						
A*0211	51	27													
A*0212	19	25		52		26	27								
A*0213	19	43		52		26	27								

Allele Number	Probe Number for Detection															
A*0214	41	13	27													
A*0216	53	27														
A*021701	54															
A*021702	19	55	24	25	13	26	56									
A*0218	57															
A*0219	58	22	59	25	52	26										
A*022001	28	60	29	21	22	23	24	30	31	32	33	25	13	26	34	
A*022002	61															
A*0221	62															
A*0222	19	20	21	22	23	24	25	44	26	27						
A*0224	28	29	20	21	22	23	24	30	31	33	25	13	26	34		
A*0225	42	25	13	26												
A*0226	19	43	13	26	27											
A*0227	22	63	52	26	34											
A*0228	64	63	25	13	34											
A*0229	65	163														
A*0230	66															
A*0231	67															
A*0233	68															
A*0234	20	69	21	22	23	24	25	12	13	26	27					
A*0235	20	69	22	23	24	30	31	32	33	25	13	26	34			
A*0236	28	29	20	21	22	23	24	30	31	32	33	25	13	26		
A*0237	22	63	25	52	26											
A*0238	63	42	52													
A*0239	50	59	70	25	13	71	26	72	34							
A*0240	63	73	74	26	34											
A*0241	46	28	29	20	21	22	23	24	75	32	33	25	13	26	34	
A*0242	76															
A*0244	46	22	25	52	26	34										

Table 4-4

Allele Number	Probe Number for Detection							
A*1103	96	97	52					
A*1104	46	69	58	52	26	72	34	
A*1105	98							
A*1106	69	21	58	52	72	34		
A*1107	99							
A*1108	46	69	58	43				
A*1109	100							
A*1110	46	82	58	52	34			
A*1111	101	58	52	34				
A*1112	46	69	58	16	52	72	34	
A*1113	102							
A*1114	95	103						
A*2301	104	13	71	105				
A*2302	77	32	73	74	44	106	26	
A*2303	31	107	73	13				
A*2304	77	32	73	74	13	71	26	72
A*2305	108	13						34
A*2306	109							
A*2309	13	71	105					
A*240201	77	110	52	111	105			
A*240202	77	110	16	55	93	31	32	52
A*240203	112							111
A*240204	113							26
A*240301	111	34	105					
A*240302	77	52	111	26	72	34		
A*2404	77	52	111	105				
A*2405	77	114	52	111	26			
A*2406	77	32	59	25	44	106	26	
A*2407	69	110	52	111	105			

Table 4-5

Allele Number	Probe Number for Detection									
A*2408	115	116								
A*2410	77	52	111	72	34					
A*2413	77	32	59	25	13	71	26			
A*2414	77	24	31	32	59	52	111	26		
A*2415	77	110	16	83	31	32	59	52	111	26
A*2417	77	110	16	55	93	32	59	52	111	26
A*2418	32	43	12	13	88					
A*2419	77	69	58	55	93	31	32	59	52	111 26
A*2420	77	110	16	55	93	31	32	59	52	111 26
A*2421	77	110	16	55	93	31	59	52	111	26
A*2422	117	34	105							
A*2423	77	52	111	26	118					
A*2424	69	55	32	73	74	13	71	26		
A*2425	108	52								
A*2426	119									
A*2427	120									
A*2428	77	58	16	55	93	31	32	59	52	111 26
A*2429	110	16	55	31	32	59	52	111	26	
A*2430	77	121	110	16	55	93	31	32	59	52 111 26
A*2431	122	25	52	26						
A*2432	123	32	52	26						
A*2433	59	25	52	26	27					
A*2434	124	52								
A*2435	125									
A*2437	126									
A*2438	127									
A*2501	123	128	129							
A*2502	69	123	128	129						
A*2503	123	42	43	44	34					

Table 4-6

Allele Number		Probe Number for Detection					
A*2504	123	43	52	34			
A*2601	82	44	128				
A*2602	130						
A*2603	21	58	44	128			
A*2604	131						
A*2605	15	44	128				
A*2606	132						
A*2607	20	44	128				
A*2608	52	128					
A*2609	133	114	42	43	26		
A*2610	32	114	42	43	44		
A*2612	114	42	25	44			
A*2613	69	133	114	42	43	44	
A*2614	46	82	133	134	43	44	
A*2615	135						
A*2616	9	82	133	114	42	43	44
A*2617	136						
A*2618	133	134	73	74	44		
A*29010101	137						
A*2902	138	34	129				
A*2903	138	129					
A*2904	139	73					
A*2905	138	52	34				
A*2906	138	13	34				
A*2907	138	55	13	34			
A*3001	9	14	140				
A*3002	10	14	141	26	34		
A*3003	10	141	26	34			
A*3004	10	25	34				

Table 4-7

Allele Number		Probe Number for Detection							
A*3006	142								
A*3007	78	141	26	34					
A*3008	46	14	140						
A*3009	10	74	13	34					
A*3010	143								
A*3011	9	140							
A*3012	14	141	26	34					
A*310102	14	107	144						
A*3102	20	51	93	133	107	73	13	34	
A*3103	51	134	73	13	34				
A*3104	134	144							
A*3105	14	51	93	133	107	73	13		
A*3106	14	51	93	107	73	13	34		
A*3107	14	110	133	107	74	13	34		
A*3108	145	77	110	133	107	13	34		
A*3109	146								
A*3201	123	13	147	129					
A*3202	123	52	147	129					
A*3203	110	148	73	13					
A*3204	123	88	149	34					
A*3205	78	123	13	147	129				
A*3206	123	25	13	26	34				
A*3207	9	123	73	74	13	26	34		
A*3301	150								
A*3303	82	107	144						
A*3304	151								
A*3305	152								
A*3306	153								
A*3401	133	43	44	26	34	154	155	129	

Table 4-8

Allele Number		Probe Number for Detection						
A*3402	43	13	26	34	154	156	155	129
A*3403	134	43	13	26				
A*3404	157	43	13	34				
A*3405	158							
A*3601	26	72						
A*3602	88							
A*3603	83	26	72	34				
A*3604	72							
A*4301	101	128	129					
A*6601	69	58	44	128				
A*6602	53	155	129					
A*6603	43	53	34					
A*6604	43	159						
A*680101	46	69	93	44	160	27		
A*680102	161	69	93	44	160	27		
A*6802	162	27						
A*680301	161	93	44	160	27			
A*680302	161	33	44					
A*6804	82	51	63	34				
A*6805	161	21	33	44				
A*6806	69	81	63	25				
A*6807	69	163	63	25				
A*6808	89	160	27					
A*6809	161	52						
A*6810	46	164	69	93	25	44	26	34
A*6812	161	69	44					
A*6813	46	69	93	44	160			
A*6814	46	164	69	93	25	44	26	34
A*6815	162	82	21					

[illegible]

(Example 3)

Probes for identification of HLA-B allele

Extraction of DNA from 1 ml of human blood was performed using GFX Genomic Blood DNA Purification
5 Kit from Amersham Biosciences in the same manner as in Example 1.

Next, quantitative PCR was carried out in the same manner as in Example 1 except that probes in the probe list B1 were used and 3 μ l of the mixed
10 primers consisting of 1 μ l each of respective solutions of the following primers (10 pmol/ μ l):

CTGAGCTCTTCCTCCTACACA (SEQ ID NO:518)

TCCTTCCCGTTCTCCAGGT (SEQ ID NO:519)

AGGTCTCGGTCAGGGCCA (SEQ ID NO:520)

15 After PCR amplification, the sample was identified being B*520101, referring to Amp Plot and Dissociation curves on a display of 5700 software and the allele-probe list B1 (described later).

(Example 4)

20 Extraction of DNA from 1 ml of human blood was performed in the same way as in Example 1. PCR of human HLA-B was then performed in the same manner as in Example 2 except that 2 μ l of the mixed primer consisting of 1 μ l each of the respective solutions
25 of the following primers at 10 pmol/ μ l and 13 μ l of ultra pure water used:

CTGAGCTCTTCCTCCTACACA (SEQ ID NO:518)

GCTCCCACTCCATGAGGTATTTTC (SEQ ID NO:521).

At the same time, a DNA microarray was prepared to identify the allele in the specimen described above in the same manner as in Example 2, except that
5 probes in the probe list B2 were to form the probe dots respectively.

Then, hybridization was performed using the above specimen and the prepared DNA microarray in the same manner as in Example 2. Fluorometry measurement
10 was conducted with GenePix4000B (Axon). Referring to the allele-probe list B2 (described later), the sample was identified as B*520101.

Allele list

15 B*070201

atgctgggtcatggcgccccgaaccgtccctcctgctgctcctggcgccccggccccgaccgagaccctgggccccgctccca
ctccatgagglatcttctacacctccGtgctcccgccccggcgccggggagccccgccttcatctcagctgggctacgtggacg
acaccagctcgtgaggttcgacagcgacgccgcgagctccgagagaggagcccgccggcgccgtggatagagcaggagggg
ccggaglatgggaccggaacacacagatctacaaggccaggcacagactgaccgagagagccctgcggaacctgcgcgg
20 ctactacaaccagagcgaggccgggtctcacacctccagagCatgtacggctgcgacgtggggccggacggcgccctcc
tccgccccCatgaccagTaccctacgacggcaaggattacatcgccctgaacgaggacctgcgctcctggaccgcccg
gacacggcggtcagatcaccagcgcaagtgggaggcgcccgctgaggcgagcagcGGagagcttacctggaggcgGA
gtgcgtggagtGgtccgcagatacctggagaacgggaaggacaagctgGagcgcgctgacccccaaagacacacgtga
cccaccaccccatctctgaccatgaggccacctgaggtgctgggccccgggttcttacctgaggagatcacactgacc
25 tggcagcgggatggcgaggaccaaactcaggacactgagcttgtggagaccagaccagcaggagatagaacctccagaa
gtgggcagctgtgtgtgtgcttctggagaagagcagagatcacatgccatgtacagcatgaggggctgccgaagcccc
tcacctgagatgggagccgtcttcccagtcaccgtccccatcgtgggcatgtgtgtggtggctgtctcttANNNgca

atgctgggcatggcgccccgaaccgtcctcctgctgctcctggcgggccclggccclgaccgagaccggcgccggcctccca
cctccatgaggtattctacacctccgigtcccgcccgccggccggggagccccgcctcatctcagtgggctacgtggacg

acacccagttcgtgaggttcgacagcgacgccgcgagtcgagagaggagccgcggcgccgtggatagagcaggagggg
ccggagtaattgggaccggaacacacagatctacaagaccaacAcacagactgaccgagagagccigcggaaacctgcgcgg
ctactacaaccagagcgaggccgggtctcacacccctcagagcatgtacggctgcgacgtggggccggacgggcgctcc
tccgcgggcatgaccagtagcctacgacggcaaggattacatcgccctgaacgaggacctgcgctcctggaccgccgcg
5 gacacggcggttcagatcacccagcgcaagtgggaggcgcccgtagggcgagcagcgagagccctaccggaggcgga
gtgcgtggagtaggtccgcagatacctggagaacgggaaggacaagctggagcgcgctgacccccaaagacacacgtga
cccaccaccccatctctgacatgaggccacctgagggtcctgggcccctgggtttctacctgcggagatcacactgacc
tggcagcgggatggcgaggaccaaactcaggacactgagcttctggagaccagaccagcaggagatagaaccttcagaa
gtgggcagctgtgggtggctctctggagaagagcagagatcacatgccatgtacagcatgaggggtgccgaagcccc
10 taccctgagatgggagccgtcttccagtcaccgtcccatctgtgggcatgtgtctggcctggctgtccta... gca
gttgtggctatcggagctgtggctgcctgtgtgtgttaggaggaagagttcaggtgga (SEQ ID NO: 525)

B*0704

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ctccatgaggtatctctacacctccgtgtcccgcccgccggcgaggccccgcttcatctcagtagggctacgtggacg
15 acacccagttcgtgaggttcgacagcgacgccgcgagtcgagagaggagccgcggcgccgtggatagagcaggagggg
ccggagtaattgggaccggaacacacagatctacaaggccaggcacagactgaccgagagagccigcggaaacctgcgcgg
ctactacaaccagagcgaggccgggtctcacacccctcagagcatgtacggctgcgacgtggggccggacgggcgctcc
tccgcgggcatgaccagtagcctacgacggcaaggattacatcgccctgaacgaggacctgcgctcctggaccgccgcg
gacacggcggttcagatcacccagcgcaagtgggaggcgcccgtagggcgagcaggaCagagccctaccggaggcgga
20 gtgcgtggagtaggtccgcagatacctggagaacgggaaggacaagctggagcgcgctgacccccaaagacacacgtga
cccaccaccccatctctgacatgaggccacctgagggtcctgggcccctgggtttctacctgcggagatcacactgacc
tggcagcgggatggcgaggaccaaactcaggacactgagcttctggagaccagaccagcaggagatagaaccttcagaa
gtgggcagctgtgggtggctctctggagaagagcagagatcacatgccatgtacagcatgaggggtgccgaagcccc
taccctgagatgggagccgtcttccagtcaccgtcccatctgtgggcatgtgtctggcctggctgtccta... gca
25 gttgtggctatcggagctgtggctgcctgtgtgtgttaggaggaagagttcaggtgga (SEQ ID NO: 526)

B*0705

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 ac|ccc|a|g|t|c|g|t|g|a|g|t|c|g|a|c|g|c|a|c|g|c|c|g|c|g|a|t|c|c|g|a|g|a|g|a|g|a|g|c|c|g|c|g|g|c|c|c|g|t|g|g|a|t|a|g|a|c|a|g|a|g|g|g|g|
 c|g|g|a|t|t|g|g|g|a|c|c|g|g|a|a|c|a|c|a|g|a|t|c|a|a|a|g|g|c|c|a|g|g|c|a|c|a|g|a|t|g|a|c|c|g|a|g|a|g|c|t|g|c|g|g|a|a|c|t|g|c|g|c|g|
 c|t|a|c|t|a|a|a|c|c|a|g|a|g|c|g|a|g|g|c|c|g|g|t|c|t|c|a|c|a|c|c|t|c|c|a|g|a|g|a|t|g|t|a|c|g|g|c|t|g|c|g|a|c|t|g|g|g|c|c|g|g|a|c|g|g|g|c|c|t|c|c|
 5 t|c|c|g|c|g|g|g|c|a|t|a|a|c|c|a|g|t|a|c|g|c|t|a|c|g|a|c|g|g|c|a|a|g|g|a|t|a|c|a|t|c|g|c|c|t|g|a|a|c|g|a|g|g|a|c|t|g|c|g|c|t|c|t|g|g|a|c|c|g|c|g|
 g|a|c|a|c|g|g|c|g|g|c|t|c|a|g|t|c|a|c|c|c|a|g|c|g|a|a|g|t|g|g|g|a|g|g|c|g|g|c|c|c|g|t|g|a|g|g|c|g|g|a|g|c|a|g|c|g|g|a|g|a|g|c|t|a|c|t|g|g|a|g|g|g|c|g|a|
 g|t|g|c|g|t|g|g|a|t|g|g|c|t|c|c|g|c|a|t|a|c|t|g|g|a|a|c|g|g|g|a|a|g|g|a|c|a|a|g|c|t|g|g|a|g|c|g|c|g|t|g|a|c|c|c|c|c|a|a|g|a|c|a|c|a|c|t|g|a|
 c|c|c|a|c|a|c|c|c|a|t|c|t|c|t|g|a|c|a|t|g|a|g|g|c|c|a|c|c|t|g|a|g|t|g|c|t|g|g|g|c|c|t|g|g|t|t|c|t|a|c|c|t|g|c|g|g|a|t|c|a|c|a|t|g|a|c|c|
 t|g|g|c|a|g|c|g|g|a|t|g|g|c|g|a|g|g|a|c|c|a|a|c|t|c|a|g|g|a|c|a|t|g|a|g|c|t|t|g|g|g|a|c|c|a|g|a|c|c|a|g|c|a|g|g|a|t|a|g|a|a|c|t|t|c|c|a|g|a|
 10 g|t|g|g|c|a|g|c|t|g|t|g|g|t|g|g|t|c|t|t|g|g|a|a|g|a|g|c|a|g|a|t|a|c|a|t|g|c|c|a|t|g|t|a|c|a|g|c|a|t|g|a|g|g|g|c|t|g|c|c|g|a|a|g|c|c|c|
 t|c|a|c|c|t|g|a|g|a|t|g|g|g|a|g|c|g|t|c|t|c|c|c|a|t|c|c|a|c|A|c|c|c|a|t|c|g|t|g|g|g|c|a|t|g|t|t|g|t|g|g|c|t|g|g|c|t|g|t|c|t|a|...g|c|a|
 g|t|t|g|t|g|g|t|a|t|c|g|g|a|g|c|t|g|t|g|t|c|g|t|g|t|g|t|g|t|g|t|g|t|g|g|g|a|a|g|a|g|t|t|c|a|g|t|g|g|a|(SEQ ID NO:527)

B*0706

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acacccagttcgtgaggttcgacagcgacgccgcgagttccgagagaggagccgcggggcgccgtggatagagcaggagggg
ccggagtattgggaccggaacacacagatctacaaggccaggcacagactgaccgagagagcctgcggaacctgcgcgg
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tccgcgggcattAaccagttacgcttacgacggcaaggattacatcgccctgaacaggagacctgcgctcctggaccgccgcg
20 gacacggcggctcagattacccagcgcaagttgggagggcgccctgaggcggagcagcggagagcctacctggagggcgga
gtgcgtggagtggctccgcagatacctggagaacgggaaggacaagctggagcgcgtgacccccaaagacacacgtga
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gtgggcagctgtgggtgggtgcttctggagaagagcagagatcacatgccatgtacagcatgaggggtgccgaagcccc
25 tccccctgagatgggagccgtcttccagttccaccgtccccatcgtgggcattgtgtcgtggccctggctgtctta... gca
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B*0707

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g|ggac|gac|acc|cag|t|c|g|gag|t|c|gac|agc|gac|ccc|g|gag|t|c|c|gag|ag|agg|ag|cc|g|c|ggg|c|g|cc|g|t|gga|t|ag|ag|ca|
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t|g|c|g|c|g|g|t|a|c|t|a|a|acc|ag|ag|c|g|agg|c|c|gg|t|c|c|ac|ccc|t|c|c|ag|ag|Ga|t|g|t|ac|gg|c|t|g|c|g|ac|t|ggg|c|c|gg|ac|ggg|
5 cg|cc|t|c|c|c|c|g|c|g|g|c|a|t|g|acc|ag|t|ac|g|c|t|ac|gac|gg|ca|agg|a|t|a|c|t|c|g|c|c|t|ga|ac|gag|g|acc|t|g|c|g|t|c|c|t|gg|ac|
cg|cc|g|c|g|g|ac|ac|gg|c|gg|t|c|aga|t|c|acc|c|ag|c|g|ca|agt|ggg|agg|c|g|g|c|c|c|t|g|agg|c|g|g|ag|c|ag|c|g|g|ag|ag|cc|t|acc|t|gg|
agg|g|c|g|ag|t|g|c|t|gg|ag|t|gg|t|c|c|g|c|aga|t|acc|t|gg|aga|ac|gg|ga|agg|aca|ag|c|t|gg|ag|c|g|c|g|t|(SEQ ID
NO:529)

B*0708

10 gg|t|cc|ac|t|cca|t|gag|ga|at|t|t|c|ac|ac|c|cc|g|t|g|ccc|ggccc|ggccg|gggag|cccc|g|t|c|at|c|c|ag|t|ggc|t|a|c|
cg|t|gg|ac|gac|acc|cag|t|c|g|t|gag|t|c|gac|agc|gac|ccc|g|gag|t|c|c|gag|ag|agg|ag|cc|g|c|ggg|c|g|cc|g|t|gga|t|ag|ag|c|
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c|t|g|c|g|c|g|t|a|c|t|a|a|acc|ag|ag|c|g|agg|c|c|gg|t|c|c|ac|ccc|t|c|c|ag|ag|ca|t|g|t|ac|gg|c|t|g|c|g|ac|t|ggg|c|c|gg|ac|gg|
g|c|g|c|t|c|c|c|c|g|c|g|g|c|a|t|g|acc|ag|t|ac|g|c|t|ac|gac|gg|ca|agg|a|t|a|c|t|c|g|c|c|t|ga|ac|gag|g|acc|t|g|c|g|t|c|c|t|gga|
15 cc|g|c|c|c|g|g|g|ac|ac|gg|c|gg|t|c|aga|t|c|acc|c|ag|c|g|ca|agt|ggg|agg|c|g|g|c|c|c|t|g|agg|c|g|g|ag|c|ag|c|g|g|ag|ag|cc|t|acc|t|g|
gag|gg|c|g|ag|t|g|c|t|gg|ag|t|gg|t|c|c|g|c|aga|t|acc|t|gg|aga|ac|gg|ga|agg|aca|ag|c|t|gg|ag|c|g|c|g|t|(SEQ ID
NO:530)

B*0709

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20 ct|cca|t|gag|ga|at|t|t|c|ac|ac|c|cc|g|t|g|ccc|ggccc|ggccg|gggag|cccc|g|t|c|at|c|c|ag|t|ggc|t|ac|t|gg|ac|g|
ac|acc|cag|t|c|g|t|gag|t|c|gac|agc|gac|ccc|g|gag|t|c|c|gag|ag|agg|ag|cc|g|c|ggg|c|g|cc|g|t|gga|t|ag|ag|cagg|agg|gg|
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t|c|c|g|g|g|c|a|t|g|acc|ag|t|C|g|c|t|ac|gac|gg|ca|agg|a|t|a|c|t|c|g|c|c|t|ga|ac|gag|g|acc|t|g|c|g|t|c|c|t|gg|acc|c|c|g|c|g|
25 gac|ac|gg|c|gg|t|c|aga|t|c|acc|c|ag|c|g|ca|agt|ggg|agg|c|g|g|c|c|c|t|g|agg|c|g|g|ag|c|ag|c|g|g|ag|ag|cc|t|acc|t|gg|agg|gg|c|ga|
g|t|g|c|t|gg|ag|t|gg|t|c|c|g|c|aga|t|acc|t|gg|aga|ac|gg|ga|agg|aca|ag|c|t|gg|ag|c|g|c|g|t|(SEQ ID NO:531)

B*0710

gctccac tccatgaggtat tctacac tccgtgtccggcccgccgaggagccccgt tcatctcag tgggtac
gtggacgacacccag ttcgtgaggttcgacagcgacgccgcgag tccgagagaggagccgaggcgccgtggatagagca
ggaggggcccggag taltgggaccggaacacacagatctGcaaggcccaggcacagac taccgagagagcc tgcggaacc
tgcgcggctac tacaaccagagcgaggccgggtctcacaccc tccagagca tgtacggc tgcgacgtggggccggacggg
5 cgcttctccgcccga taccag taccgtacgacggcaaggat taca tgccttgaacgaggacctgcgtctctggac
cgcccgggacacggcggtcagatcaccagcgcaagtgggaggcgcccg tggcgggagcagcgagagacctacc tgg
aggcgag tgcgtggag tggctccgcagat acc tggagaacgggaaggacaagc tggagcgcgctg (SEQ ID
NO:532)

B*0711

10 gctccac tccatgaggtat tctacac tccgtgtccggcccgccgaggagccccgt tcatctcag tgggtac
gtggacgacacccag ttcgtgaggttcgacagcgacgccgcgag tccgagagaggagccgaggcgccgtggatagagca
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tgcgcggctac tacaaccagagcgaggccgggtctcacaccc tccagagca tgtacggc tgcgacgtggggccggacggg
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aggcgag tgcgtggag tggctccgcagat acc tggagaacgggaaggacaagc tggagcgcgctg (SEQ ID
NO:533)

B*0712

gctccac tccatgaggtat tctacac tccgtgtccggcccgccgaggagccccgt tcatctcag tgggtac
20 gtggacgacacccag ttcgtgaggttcgacagcgacgccgcgag tccgagagaggagccgaggcgccgtggatagagca
ggaggggcccggag taltgggaccggaacacacagatctacaaggcccaggcacagac taccgagagagcc tgcggaacc
tgcgcggctac tacaaccagagcgaggccgggtctcaca tctccagaggatgtatTggc tgcgac tggggccGcacggg
cgcttctccgcccga taccag taccgtacgacggcaaggat taca tgccttgaacgaggacctgcgtctctggac
cgcccgggacacggcggtcagatcaccagcgcaagtgggaggcgcccg tggcgggagcagcgagagacctacc tgg
25 agggcgag tgcgtggag tggctccgcagat acc tggagaacgggaaggacaagc tggagcgcgctg (SEQ ID

NO:534)

B*0713

gc tcc cactcca t gaggta t t t c t a c a c c t c c g t g t c c c g g c c c g g c c g g g g a g c c c c g c t t c a t c t c a g t g g g c t a c
g t g g a c g a c a c c c a g t t c g t g a g g t t c g a c a g c g a c g c c g c g a g t c c g a g a g g g a g c c g c g g g c g c c g t g g g t g g a g c a
g g a g g g g c c g g a g t a t t g g g a c c g g g a g a c a c a g a a g t a c a a g c G c c a g g c a c a g G c t g a c c g a g T g a c c t g c g g a a c c
t g c g c g g c t a c t a c a a c c a g a g c g a g g c c g g g t c t c a c a c c t c c a g a g c a t g t a c g g c t g c g a c g t g g g c c g g a c g g g
5 c g c c t c c t c c g c g g g c a t g a c c a g t a c g c c t a c g a c g g c a a g g a t t a c a t c g c c c t g a a c g a g g a c c t g c g c t c c t g g a c
c g c c g c g g a c a c g g c g g c t c a g a t c a c c c a g c g c a a g t g g g a g g c g g c c c g t g a g g c g g a g c a g c g g a g a g c c t a c c t g g
a g g g c g a g t g c g t g g a g t g g c t c c g c a g a t a c c t g g a g a a c g g g a a g g a c a a g c t g g a g c g c g c t g (SEQ ID
NO:535)

B*0714

10 g c t c c c a c t c c a t g a g g t a t t t c t a c a c c t c c g t g t c c c g g c c c g g c c g c g g g g a g c c c c g c t t c a t c t c a g t g g g c t a c
g t g g a c g a c a c c c a g t t c g t g a g g t t c g a c a g c g a c g c c g c g a g t c c g a g a g a g g a g c c g c g g g c g c c g t g g a t a g a g c a
g g a g g g g c c g g a g t a t t g g g a c c g g a a c a c a c a g a t c t a c a a g g c c c a g g c a c a g a c t g a c c g a g a g a g c c t g c g g a a c c
t g c g c g g c t a c t a c a a c c a g a g c g a g g c c g g g t c t c a c a T c A t c c a g a g G a t g t a c g g c t g c g a c g t g g g c c g g a c g g g
c g c c t c c t c c g c g g g T a t g a c c a g t a c g c c t a c g a c g g c a a g g a t t a c a t c g c c c t g a a c g a g g a c c t g c g c t c c t g g a c
15 c g c c g c g g a c a c g g c g g c t c a g a t c a c c c a g c g c a a g t g g g a g g c g g c c c g t g a g g c g g a g c a g c g g a g a g c c t a c c t g g
a g g g c g a g t g c g t g g a g t g g c t c c g c a g a t a c c t g g a g a a c g g g a a g g a c a a g c t g g a g c g c g c t g (SEQ ID
NO:536)

B*0715

20 g c t c c c a c t c c a t g a g g t a t t t c t a c a c c t c c g t g t c c c g g c c c g g c c g c g g g g a g c c c c g c t t c a t c t c a g t g g g c t a c
g t g g a c g a c a c c c a g t t c g t g a g g t t c g a c a g c g a c g c c g c g a g t c c g a g a g a g g a g c c g c g g g c g c c g t g g a t a g a g c a
g g a g g g g c c g g a g t a t t g g g a c c g g a a c a c a c a g a t c t a c a a g g c c c a g g c a c a g G c t g a c c g a g T g a c c t g c g g a a c c
t g c g c g g c t a c t a c a a c c a g a g c g a g g c c g g g t c t c a c a c c t c c a g a g c a t g t a c g g c t g c g a c g t g g g c c g g a c g g g
c g c c t c c t c c g c g g g c a t g a c c a g t a c g c c t a c g a c g g c a a g g a t t a c a t c g c c c t g a a c g a g g a c c t g c g c t c c t g g a c
c g c c g c g g a c a c g g c g g c t c a g a t c a c c c a g c g c a a g t g g g a g g c g g c c c g t g a g g c g g a g c a g c g g a g a g c c t a c c t g g
25 a g g g c g a g t g c g t g g a g t g g c t c c g c a g a t a c c t g g a g a a c g g g a a g g a c a a g c t g g a g c g c g c t g (SEQ ID
NO:537)

B*0716

- gcctccactccatgaggatattctacacctccggtgccggcccgccggggagccccgcttcatctcagtgggctac
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ggaggggcccggagttatgggaccggaacacacagatctacaagaccaacAcacagacTaccgagagagcctgcggaacc
tgcgcggctactacaaccagagcgaggccgggtctcacacctccagagcaltgacggctgcgacgtggggccggacggg
5 cgccctctccgcccgaatgaccagttacgcttacgacggcaaggattacatcgccctgaacgaggaccctgcgtctctggac
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NO:538)
B*0717
- 10 gctccactccatgaggatattctacacctccggtgccggcccgccggggagccccgcttcatctcagtgggctac
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ggaggggcccggagttatgggaccggaacacacagatctacaaggcccaggcacagacTaccgagagagcctgcggaacc
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cgccctctccgcccgaatgaccagttacgcttacgacggcaaggattacatcgccctgaacgaggaccctgcgtctctggac
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NO:539)
B*0718
- 20 atgtggctcatggcgccccgaaccgtctctctgctctcggcgccctggccctgaccgagaccctggccggctccca
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tggcagcggga tggcaggaccaaac taggacac t agc t t t gggagac cagaccagcaggagatagaacctccagaa
gtgggcagc t g t g g t g g t g c c t t c t g g a g a g c a g a g a t a c a c a t g c c a t g t a c a g c a t g a g g g g c t g c c g a a g c c c c
t c a c c c t g a g a t g g g a g c c g t c t t c c c a g t c c a c c g t c c c c a t c g t g g g c a t t g t t g c t g g c c t g g c t g t c c t a . . . g c a
g t t g t g g t c a t c g g a g c t g t g g t c g c t g c t g t g a t g t g t a g g a g a a g a g t t c a g g t g g a (SEQ ID NO: 540)

5 B*0719

g c t c c c a c t c c a t g a g g t a t t t c t a c a c c t c c g t g t c c c g g c c c g g c c g g g g a g c c c c g t t c a t c t c a g t g g g c t a c
g t g g a c g a c a c c c a g t t c g t g a g g t t c g a c a g c g a c c c g c g a g t c c g a g a g a g g a g c c g c g g g c c c g t g g a t a g a g c a
g g a g g g g c c g g a g t a t t g g g a c c g g a a c a c a g a t c t a c a a g g c c c a g g c a c a g a c t g a c c g a g a g a g c c t g c g g a a c c
t g c g c g g c t a c t a c a a c c a g a g c g a g g c c g g g t c t c a c a c c t c c a g a g c a t g t a c g g c t g c g a c t g g g g c c g g a c g g g
10 c g c c t c c t c c g c g g g c a t g a c c a g t a c g c t a c g a c g g c a a g g a t t a c a t c g c c c t g a a c g a g g a c c t g c g c t c c t g g a c
c g c c g c g g a c a c g g c g g c t c a g a t c a c c c a g c g c a a g t g g g a g g c g g c c c g t g a g g c g g a g c a g a C a g a g c c t a c c t g g
a g g g c a C g t g c g t g g a g t g g c t c c g c a g a t a c c t g g a g a a c g g a a g g a G a c g c t g g a g c g c g c G (SEQ ID
NO: 541)

B*0720

15 g c t c c c a c t c c a t g a g g t a t t t c t a c a c c t c c g t g t c c c g g c c c g g c c g g g g a g c c c c g t t c a t c t c a g t g g g c t a c
g t g g a c g a c a c c c a g t t c g t g a g g t t c g a c a g c g a c c c g c g a g t c c g a g a g a g g a g c c g c g g g c c c g t g g a t a g a g c a
g g a g g g g c c g g a g t a t t g g g a c c g g a a c a c a g a t c t a c a a g g c c c a g g c a c a g a c t g a c c g a g a g a g c c t g c g g a a c c
t g c g c g g c t a c t a c a a c c a g a g c g a g g c c g g g t c t c a c a c c t c c a g a g c a t g t a c g g c t g c g a c t g g g g c c g g a c g g g
c g c c t c c t c c g c g g g c a t g a c c a g t a c g c t a c g a c g g c a a g g a t t a c a t c g c c c t g a a c g a g g a c c t g c g c t c c t g g a c
20 c g c c g c g g a c a c g g c g g c t c a g a t c a c c c a g c g c a a g t g g g a g g c g g c c c g t g a g g c g g a g c a g c g g a g a g c c t a c c t g g
a g g g c c T g t g c g t g g a g t C g c t c c g c a g a t a c c t g g a g a a c g g a a g g a c a a g c t g g a g c g c g c t g (SEQ ID
NO: 542)

B*0721

25 g c t c c c a c t c c a t g a g g t a t t t c t a c a c c t c c g t g t c c c g g c c c g g c c g g g g a g c T c c g c t t c a t c t c a g t g g g c t a c
g t g g a c g a c a c c c a g t t c g t g a g g t t c g a c a g c g a c c c g c g a g t c c g a g a g a g g a g c c g c g g g c c c g t g g a t a g a g c a
g g a g g g g c c g g a g t a t t g g g a c c g g a a c a c a g a t c t a c a a g g c c c a g g c a c a g a c t g a c c g a g a g a g c c t g c g g a a c c
t g c g c g g c t a c t a c a a c c a g a g c g a g g c c g g g t c t c a c a c c t c c a g a g c a t g t a c g g c t g c g a c t g g g g c c g g a c g g g

cgccctcciccgcgggcatgaccaglacgcciacgacggcaaggattacalcgcccigaacgaggaccitgcgicctggac
cgccgcggacacggcggcicagatcaccagcgcaagtgaggaggcgcccgtagggcgagcagcgagagccitaccigg
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NO:543)

5 B*0722

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ggaggggcccggaglatgggaccggaacacacagatctacaaggcccaggcacagactgaccgagagagccitcggaacc
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10 cgccctcciccgcgggcatgaccaglacgcciacgacggcaaggattacalcgcccigaacgaggaccitgcgicctggac
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NO:544)

B*0723

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ggaggggcccggaglatgggaccggaacacacagatctacaaggcccaggcacagactgaccgagagagccitcggaacc
tgcgcggcCactacaaccagagcgaggccgggtctcacacccicagagcatgtacggctgcgacitggggccggacggg
cgccctcciccgcgggcatgaccaglacgcciacgacggcaaggattacalcgcccigaacgaggaccitgcgicctggac
20 cgccgcggacacggcggcicagatcaccagcgcaagtgaggaggcgcccgtagggcgagcagcgagagccitaccigg
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NO:545)

B*0724

25 gctccactccatgaggatattc lacaccciccgigicccggcccgccgaggagccccgcttcatctcagitgggtac
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ggaggggcccggaglatgggaccggaacacacagatctacaaggcccaggcacagactgaccgagagagccitcggaacc
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cgccctccgccgggcatgaccagtagccctacgacggcaaggatlacatcgccctgaacgaggaccctgcgtccctggac
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NO:546)

5 B*0725

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ggaggggcccggagttatgggaccggaacacacagatctacaaggccaggcacagactgaccgagagagccctgcggaacc
tgccgggtactacaaccagagcgaggccgggtctcacacctccagagcatgtacggctgcgacgtggggccggacggg

10 cgccctccgccgggcatgaccagtagccctacgacggcaaggatlacatcgccctgaacgaggaccctgcgtccctggac
cgcccgccgacacggcggtcagatcacccagcgcaaglgggaggcgcccgtagggcggagcaggaCagagccctaccctgg
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NO:547)

B*0726

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20 cgcccgccgacacggcggtcagatcacccagcgcaaglgggaggcgcccgtagggcggagcagcTgagagccctaccctgg
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NO:548)

B*0727

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25 gtggacgacacccagttcgtgaggttcgacagcgacgcccgagctccgagagaggagcccgccggcgccgtggatagagca
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tgctcGctactacaaccagagcgaggccgggtctcacacctccagagcatgtacggctgcgacgtggggccggacggg

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NO:549)

5 B*0728

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ggaggggcccggagtattgggaccggaacacacagatctacaaggcccaggcacagactgaccgagagagccitcggaacc
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NO:550)

B*0729

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ggaggggcccggagtattgggaccggaacacacagatctacaaggcccaggcacagactgaccgagagagccitcggaacc
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NO:551)

B*0730

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B*0802

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B*0804

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5 B*0805

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B*0807

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5 B*0812

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5 B*0815

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B*1301

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B*1302

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B*1303

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B*1304

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5 B*1503

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B*1521

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B*1530

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B*1556

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25 N0:643)

B*1557

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B*1558

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B*1560

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25 NO: 646)

B*1561

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NO: 647)

B*1562

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NO: 648)

B*1563

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25 NO: 649)

B*1564

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NO: 650)

B*1565

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NO: 651)

B*1566

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B*1567

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NO: 653)

B*1568

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25 B*1569

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NO:655)
B*1570
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15 NO:656)
B*1571
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B*1572

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B*1573

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NO:659)

B*1574

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NO:660)

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NO:663)

B*1802

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B*1803

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B*2702

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B*3513

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NO: 721)

B*3514

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NO:729)

5 B*3522

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NO:730)

B*3523

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B*3524

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NO:732)

5 B*3525

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NO:733)

B*3526

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NO:734)

B*3527

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5 B*3528

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B*3529

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B*3530

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NO:738)

5 B*3531

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B*3532

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NO:780)

B*3533

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10 B*3534

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NO: 782)

B*3535

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NO: 783)

B*3536

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NO:784)

10 B*3537

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NO:785)g

B*3538

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B*3539

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NO:787)

B+3541

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B+3542

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[illegible]

B*3543

[illegible]

B*3544

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NO:791)

5 B*3545

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NO:792)

B*3701

[illegible]

B*3702

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5 B*390601

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B*390602

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B*3907

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B*3908

[illegible]

B*3909

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B#3910

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B*3911

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B*3912

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NO:822)

20 B*3913

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NO:823)

B*3914

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10 NO:824)

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20 B*3916

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NO:826)

B*3917

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B*3918

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NO:828)

20 B*3919

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NO:829)

B*3920

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25 B*3927

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B*4003

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B*4004

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B*4007

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25 cgcccgggacacggcggclcagaltcaccagcgcaagltTggaggcgcccgltTggcggagcagcTgagagccleccigga
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NO: 848)

B*4011

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NO:849)

10 B*4012

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acacGcagttcgtgaggttcgacagcgacgccgagltccgagagaggagccgaggcgccAtggatagagcaggagggg
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B*4013

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acacgctgttcgtgaggttcgacagcgacgccacgagltccgaggaaggagccgaggcgccatggatagagcaggagggg
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25 tccgcgggcatAaccagtacgcttacgacggcaaggattacatcgccctgaacgaggacctgcgctcttgaccgccgcg
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B*401401

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ggaggggcccggaglat|gggaccgggagacacagat|ccaagaccaacacacagact|accgagagagcc|gcggaacc
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NO:852)

10 B*401402

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NO:853)

B*4015

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ggaggggcccggaglat|gggaccgggagacacagat|ccaagaccaacacacagact|accgagagagcc|gcggaacc
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20 cgcc|cc|ccgcgggc|a|accag|acgcc|acgacggcaaggat|acal|cgccc|gaacgaggacc|gcgc|cc|tggac
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NO:854)

B*4016

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10 B*4018

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NO:856)

B*4019

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cgctccgctactacaaccagagcgaggccgggtctcacaccctccagagcatgtacggctgcgacgtggggccggacggg
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NO:857)

B#4020

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10 B#4021

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ggagggggcggtatTgggaccgggaGacacagatctCcaagaccaacacacagactTaccgagagagcctgcggaacc
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NO:859)

B#4023

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B*4024

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g t g g a c g a c a c g c t g t t c g t g a g g t t c g a c a g c g a c g c c A c g a g t c c g a g g a a g g a g c c g c g g g c g c c A t g g a t a g a g c a
g g a g g g c c g g a g t a t t g g g a c c g g g a G a c a c a g a t c t C c a a g a c c a a c A c a c a g a c t T a c c g a g a g a g c c t g c g g a a c c
5 t g c g c g g c t a c t a c a a c c a g a g c g a g g c c g g g t c t c a c a c c t c c a g a g c a t g t a c g g c t g c g a c t g g g g c c C g a c g g g
c g c t c c t c c g c g g g c a t g a c c a g t a c g c c t a c g a c g g c a a g g a t t a c a t c g c c c t g a a c g a g g a c c t g c g c t c c t g g a c
c g c c g c g g a c a c g g c g g c t c a g a t c a c c c a g c g a a g t g g g a g g c g g c c c g t g T g g c g g a g c a g c T g a g a g c c t a c c t g g
a g g g c g a g t g c g t g g a g t g g c t c c g c a g a t a c c t g g a g a a c g g g a a g g a g a c g c t g C a g c g c g c G g (S E Q I D
N O : 8 6 1)

10 B*4025

g c t c c c a c t c c a t g a g g t a t t t c C a c a c c g c c a t g t c c c g g c c c g g c c g g g g a g c c c c g c t t c a t c a c c g t g g g c t a c
g t g g a c g a c a c g c T g t t c g t g a g g t t c g a c a g c g a c g c c A c g a g t c c g a g g A a g g a g c c g c g g g c g c c A t g g a t a g a g c a
g g a g g g c c g g a g t a t t g g g a c c g g a a c a c a c a g a t c t C c a a g a c c a a c a c a c a g a c t T a c c g a g a g a g c c t g c g g a a c c
t g c g c g g c t a c t a c a a c c a g a g c g a g g c c g g g t c t c a c a c c t c c a g a g G a t g t a c g g c t g c g a c t g g g g c c g g a c g g g
15 c g c t c c t c c g c g g g c a t A a c c a g t a c g c c t a c g a c g g c a a g g a t t a c a t c g c c c t g a a c g a g g a c c t g c g c t c c t g g a c
c g c c g c g g a c a c g g c g g c t c a g a t c t c c a g c g c a a g t T g g a g g c g g c c c g t g T g g c g g a g c a g c t g a g a g c c t a c c t g g
a g g g c g a g t g c g t g g a g t g g c t c c g c a g a t a c c t g g a g a a c g g g a a g g a c a a g c t g g a g c g c g t g (S E Q I D
N O : 8 6 2)

B*4026

g c t c c c a c t c c a t g a g g t a t t t c c a c a c c t c c g t g t c c c g g c c c g g c c g g g g a g c c c c g c t t c a t c a c c g t g g g c t a c
g t g g a c g a c a c g c t g t t c g t g a g g t t c g a c a g c g a c g c c A c g a g t c c g a g g a a g g a g c c g c g g g c g c c a t g g a t a g a g c a
g g a g g g c c g g a g t a t t g g g a c c g g g a G a c a c a g a t c t C c a a g a c c a a c a c a c a g a c t T a c c g a g a g a g c c t g c g g a a c c
t g c g c g g c t a c t a c a a c c a g a g c g a g g c c g g g t c t c a c a c c t c c a g a g g a t g t a c g g c t g c g a c t g g g g c c g g a c g g g
20 c g c t c c t c c g c g g g c a t a a c c a g t a c g c c t a c g a c g g c a a A g a t t a c a t c g c c c t g a a c g a g g a c c t g a g c t c c t g g a c
c g c g g c g g a c a c g g c g g c t c a g a t c a c c c a g c g c a a g t g g g a g g c g g c c c g t g a g g c g g a g c a g c T g a g a g c c t a c c t g g
a g g g c c T g t g c g t g g a g t g g c t c c g c a g a t a c c t g g a g a a c g g g a a g g a g a c g c t g c a g c g c g c g g (S E Q I D
N O : 8 6 3)

B*4027

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ggaggggcccggagtaattgggaccgggagacacagatcccaagaccaacacacagacttaccgagagagccgtcggaacc
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NO:864)

10 B*4028

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cgcgcgacacggcggtcagatcaccagcgcaagtgaggaggcgcccggtgaggcgagcagctgagagccctacc tgg
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NO:865)

B*4029

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NO:866)

B*4030

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NO: 867)

10 B*4031

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ggagggg|ccg|gag|a|t|ggg|acc|ggg|Gacacagat|c|Ccaagaccaacacacagac|t|Taccgagagagcc|t|cggaacc
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NO: 868)

B*4032

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t|gc|cg|gct|tac|acaaccagagcgaggccggg|t|c|acaccc|t|ccagagca|t|g|t|acggc|t|gc|gac|t|ggg|cc|ggac|ggg
20 cgcc|t|c|t|ccg|ggg|c|a|gaccag|t|ac|gcc|t|acgac|ggc|aaggat|t|acat|cgccc|gaacgaggacc|t|cgct|cc|tggac
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25 agggcgag|t|gc|t|ggag|tggc|t|ccgcagat|acc|tggagaacgggaaggacaagc|tggagcgcgct|g (SEQ ID
NO: 869)

B*4033

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10 B*4034

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10 B*4037

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NO: 877)

B*4042

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ggaggggcccggagtatgggaccgggagacacagatcccaagaccaacacacagacttaccgagagaacctgcgcaccg
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25 cgcttctccgaggatgaccaggacgctacgacggcaaggattacatcgccctgaacgaggacctgagctctggac
cgcgccggacacccggtcagatcaccagcgcaagtgaggagcgcccggtgTggcgagcagctgagagccctacc tgg
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NO:919)

B*4431

a l g c g g g i c a c g g c g c c c g a a c c c t c c t c c t g c t g c t c l g g g g g c a g t g g c c c t g a c c g a g a c c t g g g c c g g t c c c a
c t c c a t g a g g t a t t t c t a c a c c g c c a t g t c c c g g c c c g g c c g g g g a g c c c c g t l c a t c a c c g t g g g c t a c g t g g a c g
5 a c a c g c t g t t c g t g a g g t t c g a c a g c g a c c c a g a g t c c g a g g a a g g a g c c g c g g g c g c c a t g g a t a g a c a g g a g g g
c c g g a g t a t t g g g a c c g g g a g a c a c a g a t c t c c a a g a c c a a c a c a c a g a c t t a c c g a g a g a a c c t g c g c a c c g c g t c c g
c t a c t a c a a c c a g a g c g a g g c c g g g t c t a c a c c c t c c a g a g g a t g t a c g g c t g c g a c g t g g g c c g g a c g g g c g c t c c
t c c g c g g g c a t a a c c a g t a c g c t a c g a c g g a a g g a t t a c a t c g c c c t g a a c g a g g a c c t g c g t c c t g g a c c g c c g c g
g a c a c g g c g g t c a g a t c t c c c a g c g a a g t g g a g g c g g c c g t g t g g c g g a g c a g t g a g a c c t a c c t g g a g g g c g a
10 g t g c g t g g a g t C g c t c c g c a g a t a c c t g g a g a a c g g a a g g a c a a g c t g g a g c g c g t g a c c c c c a a g a c a c a c g t g a
c c c a c c a c c c a t c t c t g a c c a t g a g g c c a c c t g a g g t g c t g g g c c c t g g g t t t c t a c c c t g c g g a g a t a c a c t g a c c
t g g c a g c g g g a t g g c g a g g a c c a a a c t c a g g a c a c t g a g c t t g t g g a g a c c a g a c c a g a g a t a g a a c c t c c a g a a
g t g g g c a g c t g t g g t g g t g c c t t c t g g a g a a g a c a g a g a t a c a c a t g c c a t g t a c a g a t g a g g g c t g c c g a a g c c c
t c a c c c t g a g a t g g g (SEQ ID NO:920)

15 B*4432

g c t c c c a c t c c a t g a g g t a t t t c t a c a c c g c c a t g t c c c g g c c c g g c c g g g g a g c c c c g t l c a t c a c c g t g g g c t a c
g t g g a c g a c a c g c t g t t c g t g a g g t t c g a c a g c g a c c c a g a g t c c g a g g a a g g a g c c g c g g g c g c c a t g g a t a g a c a
g g a g g g c c c g g a g t a t t g g g a c c g g a g a c a c a g a t c t c c a a g a c c a a c a c a c a g a c t t a c c g a g a g a a c c t g c g c a c c g
c g c t c c g t a c t a c a a c c a g a g c g a g g c c g g g t c t a c a t c a t c c a g a g g a t g t a c g g c t g c g a c g t g g g c c g g a c g g g
20 c g c c t c c t c c g c g g g t a t g a c c a g g a c g c c t a c g a c g g a a g g a t t a c a t c g c c c t g a a c g a g g a c c t g a g c t c c t g g a c
c g c g g c g g a c a c c g c g g c t c a g a t c a c c a g c g a a g t g g g a g g c g g c c g t g t g g c g g a g c a g t g a g a c c t a c c t g g
a g g g c c t g t g c g t g g a g t C g c t c c g c a g a t a c c t g g a g a a c g g a a g g a g a c g t g c a g c g c g c g g (SEQ ID
NO:921)

B*4433

25 g c t c c c a c t c c a t g a g g t a t t t c t a c a c c g c c a t g t c c c g g c c c g g c c g g g g a g c c c c g t l c a t c a c c g t g g g c t a c
g t g g a c g a c a c g c t g t t c g t g a g g t t c g a c a g c g a c c c a g a g t c c g a g g a a g g a g c c g c g g g c g c c a t g g a t a g a c a
g g a g g g c c c g g a g t a t t g g g a c c g g g a g a c a c a g a t c t c c a a g a c c a a c a c a c a g a c t t a c c g a g a g a a c c t g c g c a c c g

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cgcc|cc|ccgcggt|gaccaggacgcc|acgacggcaaggat|acatc|Accc|gaacgaggacct|gagc|cc|ggac
cgcgcgggacacccgcggtc|agatc|accacagcgcaag|gggaggcggcccg|g|ggcggagcaggacagagcc|acc|gg
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5 NO: 922)

B*4501

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10

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20 B*4502

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NO:924)

B*4503

gctccac tccatgaggta t tccacaccgcca t g tcccgcccgcccgccgggagccccgct tca taccgtgggtac
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cgcc t c c tcccggg t a t a a c c G g t a g c c t a c g a c g g c a a g g a t t a c a t c g c c c t g a a c g a g g a c c t g a g c t c c t g g a c
cgcgcgacaccgcggt c a g a l c a c c c a g c g c a a g t g g g a g g c g c c c g t g t g g c g g a g c a g a c a g a g c c t a c c t g g
agggcc t g t g c t g g a g t c g c t c c g c a g a t a c c t g g a g a a c g g g a a g g a g a c g c t g c a g c g c g c g g (SEQ ID

10 NO:925)

B*4504

a t g c g g g t c a c g g c a c c c c g a a c c g t c c t c c t g c t g c t c t c g g c g g c c c t g g c c c t g a c c g a g a c c t g g g c c g g c t c c c a
c t c c a t g a g g t a t t t c c a c a c c g c c a t g t c c c g g c c c g g c c g g g g a g c c c c g c t t c a t c a c c g t g g g t a c g t g g a c g
a c a c g c t g t t c g t g a g g t c g a c a g c g a c c c a c g a g t c c g a g g a a g g a g c c g c g g g c g c c a t g g a t a g a c a g g a g g g
15 c c g g a g t a t t g g g a c c g g g a g a c a c a g a t c t c c a a g a c c a a c a c a c a g a c t t a c c g a g a g a c c t g c g g a a c c t g c g c g g
c t a c t a c a a c c a g a g c g a g g c c g g t c t c a c a c t t g g c a g a g g a t g t a t g g c t g c g a c c t g g g g c c g a c g g g c g c c t c c
t c c g c g g g T a t a a c c a g t t A g c c t a c g a c g g c a a g g a t t a c a t c g c c c t g a a c g a g g a c c t g a g c t c c t g g a c c g c g c g
g a c a c c g c g g c t c a g a l c a c c c a g c g c a a g t g g g a g g c g g c c c g t g t g g c g g a g c a g a C a g a g c c t a c c t g g a g g c c t
g t g c g t g g a g t g g c t c c g c a g a t a c c t g g a g a a c g g g a a g g a g a c g c t g c a g c g c g c g g a c c c c c a a g a c a c a t g t g a
20 c c c a c c a c c c a t c t c t g a c c a t g a g g c c a c c t g a g g t g c t g g g c c c t g g g c t t c t a c c c t g c g g a g a l c a c a c t g a c c
t g g c a g c g g g a t g g c g a g g a c c a a a c t c a g g a c a c C g a g c t t g t g g a g a c c a g a c c a g c a g g a g a t a g a a c c t t c c a g a a
g t g g g c a g c t g t g g t g g t g c c t t c t g g a g a g a g c a g a g a t a c a c a t g c c a t g t a c a g c a t g a g g g c t g c c g a a g c c c c
t c a c c c t g a g a t g g g a g c c a l c t t c c c a g t c c a c c a t c c c c a t c g t g g g c a t t g t t g c t g g c c t g g c t g t c c t a . . . g c a
g t t g t g g t a c t c g g a g c t g t g g t c g c t A c t g t a t g t g t a g g a g a a g a g C t c a g g t g g a (SEQ ID NO:926)

25 B*4505

g c t c c c a c t c c a t g a g g t a t t t c c a c a c c g c c a t g t c c c g g c c c g g c c g g g g a g c c c c g c t t c a t c a c c g t g g g c t a c
g t g g a c g a c a c g c t g t t c g t g a g g t c g a c a g c g a c c c a c g a g t c c g a g g a a g g a g c c g c g g g c g c c a t g g a t a g a g c a

ggaggggcccggaglatlgggaccgggagacacagatlcaccaagaccaacacacagac laccgagagagcc lgcggaacc
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cgcgccggacaccgcggclcagatcaccagcgcaag lgggaggcgcccgl lggcggagcaggacagagTctacc lgg
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B*4506
gc lccac lcca laggat lccacaccgcca lglcccggcccggccgaggagccccgc lca laccglgggclac
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NO:928)
15 B*4601
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NO: 930)

[illegible]

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B+4703
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NO:933)
20 B+4704
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B*4803

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NO:937)

B*4804

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B*4805

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20 gtgggcagctgtggtaggtgcttcttgagaagagcagagatcacatgccatgtacagcatgaggggctccgaagcccc
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B#5105

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25 g tggac gacacc cag t t c g tggg t t c gacag cgac gccgc gag t c gaggac ggag cccgggc cca tggat agag ca
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B*5106

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NO:959)

B*5107

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25 NO:960)

B*5108

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B*5109
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B*5110
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5 B*5112

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NO:964)

B*511301

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 20 cgcgccggacacccgggTcagatcaccagcgcaaglgggaggcgcccgTgaggcgagcagTgagagcctaccTgg
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NO:965)

B*511302

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NO:966)

5 B*5114

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NO:967)

B*5115

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NO:968)

B*5116

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NO:969)

5 B*5117

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NO:970)

B*5118

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NO:971)

B*5119

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NO:972)

5 B*5120

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NO:973)

B*5121

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NO:974)

B*5122

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NO: 975)

5 B*5123

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NO: 976)

B*5124

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NO: 977)

B*5126

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NO: 978)

5 B*5128

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NO: 979)

B*5129

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25 aagccccctacccctgagatggg (SEQ ID NO: 980)

B*5130

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B*5204

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B+5502

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B*5503

5 g|c|ccc|ac|l|c|a|gag|g|a|t|t|c|l|ac|cc|g|c|c|a|g|l|c|c|c|g|g|c|c|g|g|c|c|g|g|g|g|g|a|g|c|c|c|g|c|l|c|a|l|c|g|c|a|g|t|gg|g|c|l|a|c|
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NO:1007)

B*5504

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15 g|t|gg|ac|g|a|c|a|c|G|c|a|g|t|c|g|t|gag|g|t|c|g|a|c|g|c|g|a|c|c|c|g|c|g|a|g|t|c|c|g|a|g|a|g|g|a|g|c|c|g|g|g|c|c|c|g|t|g|g|a|l|a|g|a|c|a|
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NO:1008)

B*5505

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c|l|c|a|l|gag|g|a|t|t|t|c|l|ac|cc|g|c|c|a|g|l|c|c|c|g|g|c|c|g|g|c|c|g|g|g|g|g|a|g|c|c|c|g|c|l|c|a|l|c|g|c|a|g|t|gg|g|c|l|a|c|t|g|g|a|c|g|
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[illegible]

gc|ccac|ccat|gagg|at|t|c|acac|cgcc|A|g|t|ccc|ggccc|ggcc|g|ggg|ag|cccc|g|c|t|c|c|G|c|ag|t|ggg|c|t|a|c|
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5 cg|cc|t|c|t|cc|g|c|ggg|c|a|a|acc|ag|t|A|g|cc|t|ac|g|ac|g|g|c|a|agg|a|t|a|c|a|t|c|g|ccc|t|g|a|ac|g|agg|acc|t|g|ag|c|t|c|t|gg|ac|
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NO:1012)

B*5510

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15 cg|c|gg|c|gg|ac|ac|c|g|c|gg|c|t|c|ag|a|t|c|a|ccc|ag|c|g|c|a|a|g|t|ggg|agg|c|g|g|ccc|g|t|T|gg|c|gg|ag|c|ag|c|t|g|ag|ag|cc|t|acc|t|gg|
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NO:1013)

B*5511

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25 aggg|c|a|C|g|t|g|c|t|gg|ag|t|gg|c|t|c|g|c|aga|t|acc|t|gg|aga|ac|ggg|a|agg|ag|ac|g|c|t|g|c|ag|c|g|c|Gg|(SEQ ID
NO:1014)

B*5512

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B*5601
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B+5602

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15 B+5603

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B*5604

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B*5605

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ggaggggcccggaglatlgggaccggaacacacagatclacaaggcccaggcacagac taccgagagagcc tgcggaacc
15 tgcgcggctac tacaaccagagcgaggccgggtctcacacttggcagaCga tglTggctgcgacgtggggccggacggg
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cgcgggcgacaccgcggtcagatcaccagcgcaagltgggaggcgccccgtTggcgagcagcTgagagcc tacc tgg
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NO:1020)

20 B*5606

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ggaggggcccggaglatlgggaccggaacacacagatclacaaggcccaggcacagac taccgagagagcc tgcggaacc
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25 cgcc tcc tccgcgggcataaaccagltacgctacgacggcaaAgat taca tgccttgaacgaggacctgAgctcttggac
cgcgggcgacaccgcggtcagatcaccagcgcaagltgggaggcgccccgtTggcgagcagcTgagagcc tacc tgg
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NO:1021)

B*5607

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5 ggaggggcccggagtagtagggaccggaacacacagatctacaaggccaggcacagactgaccgagagaacctgcgcACcg
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10 NO:1022)

B*5608

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NO:1023)

20 B*5609

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25 cgcttctccgcccgaatgaccagtagccctacgacggcaaggatctacatcgcccgaacgaggacctgAgctcttggac
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NO:1024)

B*5610

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g|gg|ac|gac|ac|G|cag|t|c|g|t|gag|t|c|g|ac|ag|c|g|ac|ccc|g|c|g|ag|t|c|c|g|ag|ag|agg|ag|c|c|g|c|gg|g|c|c|c|t|g|g|a|t|ag|ag|ca
5 gg|gg|gg|gg|c|c|g|g|ag|t|a|t|gg|g|ac|c|g|ga|ac|ac|ac|ag|a|t|c|t|a|a|agg|ccc|agg|c|ac|ag|ac|t|g|ac|c|g|ag|ag|ag|c|t|g|c|g|ga|aac
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cg|cc|t|cc|t|cc|g|c|gg|g|c|a|t|aac|cag|t|t|Ag|cc|t|ac|g|ac|gg|c|a|agg|a|t|a|c|a|t|c|g|ccc|t|g|aac|g|agg|ac|c|t|g|ag|c|t|c|t|gg|ac
cg|cg|cg|gg|ac|acc|cg|gg|t|c|ag|a|t|c|acc|c|ag|c|g|ca|ag|t|gg|g|ag|g|c|gg|ccc|t|g|T|gg|c|g|g|ag|c|ag|t|g|ag|ag|c|t|acc|t|gg
agg|g|c|a|C|g|t|g|c|t|gg|ag|t|gg|t|c|c|g|c|ag|a|t|acc|t|gg|aga|ac|gg|ga|agg|ag|ac|gc|t|g|c|ag|c|g|c|g|C|g|(SEQ ID

10 NO:1025)

B*5611

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c|t|cca|t|gag|g|t|a|t|t|c|t|ac|acc|g|cca|t|g|t|ccc|gg|ccc|gg|c|c|g|gg|g|g|ag|cccc|g|t|c|a|t|c|g|c|ag|t|gg|g|t|ac|g|t|gg|ac|g
ac|ac|gc|ag|t|c|g|t|gag|t|c|g|ac|ag|c|g|ac|ccc|g|c|g|ag|t|c|c|g|ag|ag|agg|ag|c|c|g|c|gg|g|c|c|c|t|g|g|a|t|ag|ag|c|agg|agg|gg|g
15 cc|gg|ag|t|a|t|gg|g|ac|c|g|ga|ac|ac|ac|ag|a|t|c|t|a|a|agg|ccc|agg|c|ac|ag|ac|t|g|ac|c|g|ag|ag|ag|c|t|g|c|g|ga|aac|t|g|c|g|c|g|g
c|t|a|c|t|a|a|acc|ag|ag|c|g|agg|c|c|gg|t|c|c|a|c|t|c|a|c|t|c|c|ag|ag|ga|t|g|t|at|gg|c|t|g|c|g|acc|t|gg|gg|ccc|G|ag|c|gg|g|c|ccc|t|c|c
t|cc|g|gg|g|c|a|t|g|acc|ag|t|T|g|ccc|t|ac|g|ac|gg|c|a|agg|a|t|a|c|a|t|c|g|ccc|t|g|aac|g|agg|ac|c|t|g|ag|c|t|c|t|gg|acc|g|c|gg|c|g
g|ac|ac|C|g|c|gg|t|c|ag|a|t|c|acc|c|ag|c|g|ca|ag|t|gg|g|ag|g|c|gg|ccc|t|g|T|gg|c|g|g|ag|c|ag|t|g|ag|ag|c|t|acc|t|gg|agg|gg|c|t|T
g|t|g|c|t|gg|ag|t|gg|t|c|c|g|c|ag|a|t|acc|t|gg|aga|ac|gg|ga|agg|ag|ac|gc|t|g|c|ag|c|g|c|g|g|ac|cccc|c|aa|g|ac|ac|ac|g|t|ga
20 ccc|acc|ac|cccc|a|t|c|t|c|t|g|acca|t|g|agg|cc|acc|t|g|agg|t|g|c|t|gg|gg|ccc|t|gg|g|C|t|t|c|t|acc|t|t|g|c|g|g|ag|a|t|ac|ac|t|g|acc
t|gg|c|ag|c|gg|ga|t|gg|c|g|agg|ac|caa|ac|t|c|agg|ac|ac|t|g|ag|c|t|t|g|t|gg|ag|acc|ag|acc|ag|c|ag|g|aga|t|aga|ac|t|t|c|c|ag|aa
g|t|gg|g|c|ag|c|t|g|t|gg|t|gg|t|g|c|t|t|c|t|gg|aga|ag|ag|c|ag|ag|a|t|ac|ac|a|t|g|cca|t|g|t|ac|ag|c|a|t|g|agg|gg|c|t|g|c|c|ga|ag|cccc
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B*570101

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c|t|cca|t|gag|g|t|a|t|t|c|t|ac|acc|g|cca|t|g|t|ccc|gg|ccc|gg|c|c|g|gg|g|g|ag|cccc|g|t|c|a|t|c|g|c|ag|t|gg|g|t|ac|g|t|gg|ac|g
ac|acc|c|ag|t|c|g|t|gag|t|c|g|ac|ag|c|g|ac|ccc|g|c|g|ag|t|c|c|g|ag|ga|t|gg|c|c|ccc|gg|g|c|g|cca|t|g|g|a|t|ag|ag|c|agg|agg|gg|g

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gacacggcggc l cagatcaccagcgcaag l gggagggcgcccg l g l g g c g g a g c a g c T g a g a g c c l a c c l g g a g g g c c l
5 g l g c g t g g a g l g g c l c c g c a g a l a c c l g g a g a a c g g a a g g a g a c g c t g c a g c g c g g a c c c c c a a g a c a c a t g l g a
cccaccaccccatc l c t g a c c a l g a g g c c a c c c l g a g g l g c t g g g c c c l g g g c l l c t a c c c l g c g g a g a l c a c a c t g a c c
l g g c a g c g g g a t g g c g a g g a c c a a a c l c a g g a c a c c g a g c l g l g g a g a c c a g a c c a g c a g g a g a l a g a a c c l c c a g a a
g l g g g c a g c l g t g g l g g l g c c l l c t g g a g a a g a g c a g a g a l a c a c a t g c c a t g l a c a g c a l g a g g g c t g c c a a g c c c c
l c a c c c l g a g a t g g g a g c c a t c l l c c c a A l c c a c c g l c c c c a t c g l g g g c a l l g t l g c l g g c c t g g c l g l c c t a . . . g c a
10 g l l g t g g l c a t c g g a g c t g t g g l g c l g c l g l g a l g l g l a g g a g a a g a g c t c a g g t g g a (SEQ ID NO: 1027)
B*570102
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g l g g a c g a c a c c c a g l l c g l g a g g l l c g a c a g c g a c c c g c g a g l c c g a g g a t g g c g c c c c g g g c c c a l g g a l a g a g c a
g g a g g g c c g g a g l a l t g g g a c g g g g a g a c a c g g a a c a l g a a g g c c l c c g c g c a g a c l t a c c g a g a g a a c c l g c g g a t c g
15 c g c l c c g c l a c t a c a a c c a g a g c g a g g c c g g g l c l c a c a l c a l c c a g g l g a l g l a l g g c t g c g a c g t g g g g c c g g a c g g g
c g c c t c c t c c g c g g g c a l g a c c a g l c T g c c t a c g a c g g c a a g g a l l a c a l c g c c c l g a a c g a g g a c c l g a g c l c c t g g a c
c g c g g c g g a c a c g g c g g c l c a g a l c a c c a g c g c a a g l g g g a g g c g g c c g l g l g g c g g a g c a g c t g a g a g c c l a c c l g g
a g g g c c l g t g c g l g g a g l g g c l c c g c a g a l a c c l g g a g a a c g g a a g g a g a c g c t g c a g c g c g c g g (SEQ ID
NO: 1028)
20 B*5702
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c l c c a t g a g g l a l l l c t a c a c c g c c a l g l c c c g g c c c g g c c g g g g a g c c c c g c l l c a t c g c a g l g g g c l a c g l g g a c g
a c a c c c a g l l c g l g a g g l l c g a c a g c g a c c c g c g a g l c c g a g g a l g g c g c c c c g g g c c c a l g g a l a g a g c a g g a g g g
c c g g a g l a l t g g g a c g g g g a g a c a c g g a a c a l g a a g g c c l c c g c g c a g a c l t a c c g a g a g a a c c l g c g g a t c g c g c l c c g
25 c t a c t a c a a c c a g a g c g a g g c c g g g l c l c a c a l c a l c c a g g l g a l g l a t g g c t g c g a c g t g g g g c c g g a c g g g c c c l c c
l c c g c g g g c a l A a c c a g l a c g c c l a c g a c g g c a a g g a l l a c a l c g c c c l g a a c g a g g a c c l g a g c l c c l g g a c c g c g g c g
g a c a c g g c g g c l c a g a l c a c c a g c g c a a g l g g g a g g c g g c c c g l g l g g c g g a g c a g c g g a g a g c c l a c c l g g a g g g c c l

gigcgtggagtggtccgcagataccitggagaacgggaaggagacgcigcagcgcgcggacccccaaagacacatgiga
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5 taccctgagatgggagccatcttcccaAtccaccgtccccaatcgiggcattgttgcitggcctggctgtctta... gca
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B*570301

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10 acaccagtlcgtgaggttcgacagcgacgccgcgagtcaggagatggcggcccgggcgccatggatagagcaggagggg
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20 gttgggtacatcgagcgtgggtgcgtgctgtgagtgtgtaggaggaagagctcaggtagga (SEQ ID NO:1030)
B*570302

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25 cgctccgtactacaaccagagcaggccgggtctcacatcatccaggtagtattggctgcgacgtggggccggacggg
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B*5704

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10 cgttcgc tacc taca accag agc gaggc cgggtctc acatcatcc agGtga tglatggc tgcgac gtgggg ccggac cggg
cgcc tctcc gcggg tatg accag Gacgcc taccag cgca aggat taca tgcgcc tgaac gaggac ttgag ctctgg ac
cgcg gcggac acggc ggtc agat cacc agcg caagtggg aggcgg ccgtgtggc ggagc agcgg agagcc tacc tgg
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NO:1032)

15 B*5705

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NO: 1033)

B*5706

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c l c c a l g a g g l a t t l c t a c a c c g c c a l g t c c c g g c c c g g c c g g g g a g c c c c g c t l c a l c g c a g l g g g c l a c g l g g a c g
a c a c c c a g l l c g t g a g g l l c g a c a g c g a c c c c g c a g l c c g a g a l g g c g c c c g g g c g c c a l g g a l a g a g c a g g a g g g g

c c g g a g l a l t g g g a c g g g g a g a c a c g g a a c a l g a a g g c c l c c g c g c a g a c t l a c c g a g a g a a c c l g c g g a l c g c g c l c c g
c l a c l a c a a c c a g a g c g a g g c c g g g t c l c a c a l c a l c c a g g l g a t g l a t g g c l g c g a c g l g g g c c g g a c g g g c g c c l c c
l c c g c g g g c a l g a c c a g l c c g c c l a c g a c g g c a a g g a t l a c a l c g c c c l g a a c g a g g a c c l g a g c l c c l g g a c c g c g g c
g a c a c g g c g g c l c a g a l c a T c c a g c g c a a g l g g g a g g c g g c c c g t g t g g c g g a g c a g c l g a g a g c c l a c c l g g a g g g c c t
5 g l g c g l g g a g l g g c l c c g c a g a l a c c l g g a g a a c g g g a a g g a g a c g c l g c a g c g c g c g g a c c c c c a a g a c a c a t g l g a
c c c a c c a c c c a l c l c l g a c c a l g a g g c c a c c c l g a g g l g c l g g g c c c l g g g c l l c l a c c c l g c g g a g a l c a c a c l g a c c
l g g c a g c g g g a l g g c g a g g a c c a a a c l c a g g a c a c c g a g c l l g l g g a g a c c a g a c c a g c a g g a g a l a g a a c c l l c c a g a a
g l g g g c a g c l g l g g l g g l g c c l l c l g g a g a g a g c a g a g a l a c a c a l g c c a t g l a c a g c a l g a g g g g c l g c c a a g c c c c
l c a c c c l g a g a l g g g a g c c a t c l l c c c a a l c c a c c g l c c c c a l c g l g g g c a l l g t l g c l g g c c l g g c l g t c c l a . . . g c a
10 g l t g l g g l c a l c g g a g c l g t g g l c g c t g c t g t a t g l g l a g g a g g a a g a g c l c a g g l g g a (S E Q I D N O : 1035)
B+5707
g c l c c c a c t c c a l g a g g l a l l t c l a c a c c g c c a t g l c c c g g c c c g g c c g g g g a g c c c c g c l l c a l c g c a g l g g g c l a c
g l g g a c g a c a c c c a g l l c g l g a g g l l c g a c a g c g a c g c c g c g a g l c c g a g g a l g g c g c c c c g g g c g c c a t g g a t a g a g c a
g g a g g g g c c g g a g l a l l g g g a c g g g g a g a c a c g g a a c a l g a a g g c c l c c g c g c a g a c t l a c c g a g a g a a c c l g c g g a l c g
15 c g c l c c g c l a c l a c a a c c a g a g c g a g g c c g g g t c l c a c a l c a l c c a g g l g a t g l a t g g c l g c g a c g l g g g c c g g a c g g g
c g c c l c c l c c g c g g g c a l a a c c a g l a c g c c l a c g a c g g c a a g g a l l a c a l c g c c c l g a a c g a g g a c c l g a g c l c c l g g a c
c g c g g c g g a c a c g g c g g c l c a g a l c a c c a g c g c a a g l g g g a g g c g g c c c g t g l g g c g g a g c a g c l g a g a g c c l a c c l g g
a g g g c c l g t g c g l g g a g l C g c l c c g c a g a l a c c l g g a g a a c g g g a a g g a g a c g c l g c a g c g c g G (S E Q I D
N O : 1035)
20 B+5708
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g l g g a c g a c a c c c a g l l c g l g a g g l l c g a c a g c g a c g c c g c g a g l c c g a g g a l g g c g c c c c g g g c g c c a t g g a t a g a g c a
g g a g g g g c c g g a g l a l l g g g a c g g g g a g a c a c g g a a c a l g a a g g c c l c c g c g c a g a c t l a c c g a g a g a a c c l g c g g a l c g
c g c l c c C c l a c l a c a a c c a g a g c g a g g c c g g g t c l c a c a l c a l c c a g g l g a t g l a t g g c l g c g a c g l g g g c c g g a c g g g
25 c g c c l c c l c c g c g g g c a l g a c c a g l c c g c c l a c g a c g g c a a g g a l l a c a l c g c c c l g a a c g a g g a c c l g a g c l c c l g g a c
c g c g g c g g a c a c g g c g g c l c a g a l c a c c a g c g c a a g l g g g a g g c g g c c c g t g l g g c g g a g c a g c l g a g a g c c l a c c l g g
a g g g c c l g t g c g l g g a g l g g c l c c g c a g a l a c c l g g a g a a c g g g a a g g a g a c g c l g c a g c g c g g (S E Q I D
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NO:1036)

B*5709

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10 NO:) 1037

B*5801

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B*5807

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20 NO:1043)

B*5901

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B*670101

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20 atgcgggicacggcgccccgaaccgicctccigcigcictggggggcagtgggccctgaccgagacctgggccggciccca
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5. B*780202

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NO: 1051)

B*7803

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NO: 1052)

B*7804

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B*7805
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NO:1054)
B*8101
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B*8201

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B*8202

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15 ctccatgaggtatctacaccgctaigtccggcccgccggggagccccgcttcaatcagtgggctacgtggacg
acacgcagttcgtgaggttcgacagcgaccccgagtcgagagaggagcccgggcgccgtggatagagcaggagggg
ccggaglatgggaccggaacacacagatctacaaggccaggcacagacigaccgagagagccigcggaaacctgcgcgg
ctactacaaccagagcgaggccgggtctcacacccctccagaggatgttggctgcgaccigggggccgacggcgccctcc
tccgcgggcataaaccagtagcctacgacggcaaggattacatcgccctgaacgaggacctagcttctggaccgcgcg
20 gacaccgcggtcagatcaccagcgcaagtgaggagcgcccgctgtggcgagcaggacagagccctacciggaggccct
gtgcgtggagtcgtccgcagatacciggagaacgggaaggagacgcigcagcgcgcgacccccaaagacacatgtga
cccaccaccccatctctgaccaigaggccacctgaggtgtcggggccctgggcttctacccigcgagatcacatgacc
tggcagcgggatggcgaggaccaaacctcaggacaccgagctgtggagaccagaccagcaggagatagaacctccagaa
gtgggcagcigtgtgggtgccttcggagaagagcagagatcacatgccatgtacagcatgagggcgccgaagcccc
25 tcacccigagatgggagccatctccagtcaccatcccatcgtgggcatgtgtcgtggcctggctgtccta... gca
gtgtgggtcatcggagcigtgggtgctacgtgtgtgtgtaggaggaagagctcaggtgga (SEQ ID NO:1057)

B*8301

aTgcgggTcacggcgccccgaacccTccTccTgcTgcTcTggggggcaGiggccctgaccgagacctgggcccgtccca
cTccatgagglattTctacaccgccATgtccggccccggccggggagccccgclTcaTcTcagTgggTlacTgggacg
acacccagTtcgTgaggtTcgacagcgacgccgcgagTccgagagaggagccgcgggcgcgTggatagagcaggagggg
ccggagTatTgggaccggaacacacagatTacaaggcccaggcacagacTgaccgagagagccTgcggaaccTgcgcgg
5 cTactacaaccagagcgaggccgggTcTcacatcAtccagaggatTlacggcTgcgacTggggccggacggcgccTcc
TccgcgggTatgaccagGacgcTlacgacggcaaggattacaTcgcctTgaacgaggaccTgagTccTggaccgcggcg
gacaccgcggcTcagatcaccagcgcaagTgggaggcgcccgTgTggcgagcaggaCagagccTaccTggaggccT
gTgcgTggagTcgTccgcagataccTggagaacgggaaggagacgcTgcagcgcgGg(SEQ ID NO:1058)

10 The following Tables 5-1 to 5-9 show Probe list
B1, and Tables 6-1 to 6-8 show Probe list B2. The
Allele-probe list is shown in Tables 7 and 8.

Table 5-1

Probe No.	Base Sequence
0	agg tat ttc tac acc tcc G (SEQ ID No: 1)
1	ct cac acc ctc cag agC (SEQ ID No: 2)
2	gc ctc ctc cgc ggg C (SEQ ID No: 3)
3	c cgc ggg cat gac cag T (SEQ ID No: 4)
4	gt gag gcg gag cag cG (SEQ ID No: 5)
5	t gag gcg gag cag cG (SEQ ID No: 6)
6	gcc tac ctg gag ggc gA (SEQ ID No: 7)
7	ggc gag tgc gtg gag tG (SEQ ID No: 8)
8	c ggg aag gac aag ctg G (SEQ ID No: 9)
9	g gag tgg ctc cgc agG (SEQ ID No: 10)
10	gc tac gtg gac gac acG (SEQ ID No: 11)
11	a cag atc tac aag acc aac A (SEQ ID No: 12)
12	gt gag gcg gag cag gaC (SEQ ID No: 13)
13	c ctc ctc cgc ggg cat A (SEQ ID No: 14)
14	cg tct tcc cag tcc acc A (SEQ ID No: 15)
15	ct cac acc ctc cag agG (SEQ ID No: 16)
16	ac cgg aac aca cag atc tT (SEQ ID No: 17)
17	a cag atc ttc aag acc aac A (SEQ ID No: 18)
18	cgc ggg cat gac cag tC (SEQ ID No: 19)
19	c cgg aac aca cag atc tG (SEQ ID No: 20)
20	ca cag act gac cga gag aA (SEQ ID No: 21)
21	g gcc ggg tct cac atc A (SEQ ID No: 22)
22	ac atc atc cag agg atg taT (SEQ ID No: 23)
23	gg atg tat ggc tgc gac C (SEQ ID No: 24)
24	c tgc gac ctg ggg ccC (SEQ ID No: 25)
25	ag aca cag aag tac aag cG (SEQ ID No: 26)
26	c aag cgc cag gca cag G (SEQ ID No: 27)
27	gca cag gct gac cga gT (SEQ ID No: 28)
28	gag gcc ggg tct cac aT (SEQ ID No: 29)
29	g tct cac atc atc cag agG (SEQ ID No: 30)
30	cgc ctc ctc cgc ggg T (SEQ ID No: 31)

Table 5-2

Probe No.	Base Sequence
31	c aag gcc cag gca cag G (SEQ ID No:32)
32	c aag acc aac aca cag act T (SEQ ID No:33)
33	cgc ggg tat gac cag tC (SEQ ID No:34)
34	gcc tac ctg gag ggc aC (SEQ ID No:35)
35	ctg gag aac ggg aag gaG (SEQ ID No:36)
36	g acg ctg gag cgc gcG (SEQ ID No:37)
37	gcc tac ctg gag ggc cT (SEQ ID No:38)
38	ggc ctg tgc gtg gag tC (SEQ ID No:39)
39	c ggc cgc ggg gag cT (SEQ ID No:40)
40	tcc tgg acc gcc gcg A (SEQ ID No:41)
41	cgg aac ctg cgc ggc C (SEQ ID No:42)
42	gcc tac ctg gag ggc C (SEQ ID No:43)
43	gg gag gcg gcc cgt gT (SEQ ID No:44)
44	gt gtg gcg gag cag gaC (SEQ ID No:45)
45	cgt gag gcg gag cag cT (SEQ ID No:46)
46	c cgg aac aca cag atc tC (SEQ ID No:47)
47	ca cag act tac cga gag G (SEQ ID No:48)
48	ctg cgg acc ctg ctC C (SEQ ID No:49)
49	c cgc ggg tat gac cag G (SEQ ID No:50)
50	cac tcc atg agg tat ttc G (SEQ ID No:51)
51	gg tat ttc gac acc gcc A (SEQ ID No:52)
52	cg aga gag gag ccg cC (SEQ ID No:53)
53	a gcc tac ctg gag ggc A (SEQ ID No:54)
54	g atg tgt agg agg aag agC (SEQ ID No:55)
55	ctg cgc acc gcg ctC C (SEQ ID No:56)
56	c cga gag aac ctg cgg aT (SEQ ID No:57)
57	gag aac ctg cgg atc gC (SEQ ID No:58)
58	ctg cgg atc gcg ctC C (SEQ ID No:59)
59	c acg ctg gag cgc gcG (SEQ ID No:60)
60	g gac cgg aac aca cag aC (SEQ ID No:61)

Table 5-3

Probe No.	Base Sequence
61	c act tgg cag acg atg taT (SEQ ID No:62)
62	g gag tat tgg gac cgg G (SEQ ID No:63)
63	c cgg gac aca cag atc tT (SEQ ID No:64)
64	cgt gtg gcg gag cag cT (SEQ ID No:65)
65	cgc ggg tac cac cag G (SEQ ID No:66)
66	c aca cag act gac cga gT (SEQ ID No:67)
67	ttc aag acc aac aca cag G (SEQ ID No:68)
68	c cgg gag aca cag atc tC (SEQ ID No:69)
69	g tgc tgg gcc ctg ggC (SEQ ID No:70)
70	g gct cag atc acc cag cT (SEQ ID No:71)
71	g tct cac act tgg cag aC (SEQ ID No:72)
72	cgc ggg cat aac cag ttA (SEQ ID No:73)
73	cg atg tat ggc tgc gac C (SEQ ID No:74)
74	tgg gag cca tct tcc caA (SEQ ID No:75)
75	gag cag ctg aga gcc tG (SEQ ID No:76)
76	gg tct cac acc ctc cag T (SEQ ID No:77)
77	cc aga cca gca gga gaC (SEQ ID No:78)
78	cc ctg aga tgg gag caA (SEQ ID No:79)
79	c atg agg tat ttc tac acc G (SEQ ID No:80)
80	c tcc cac tcc atg agg C (SEQ ID No:81)
81	g cag gag ggg ccg gaA (SEQ ID No:82)
82	g gag tgg ctc cgc aga C (SEQ ID No:83)
83	g acg ctg cag cgc gcG (SEQ ID No:84)
84	c acc ctc cag agg atg taT (SEQ ID No:85)
85	tc ctg ctg ctc tcg ggA (SEQ ID No:86)
86	gcg ccc cgg gcg ccA (SEQ ID No:87)
87	gag tat tgg gac cgg gaG (SEQ ID No:88)
88	c cgt gag gcg gag cag T (SEQ ID No:89)
89	gac caa act cag gac acC (SEQ ID No:90)
90	cc gcc tac gac ggc aaA (SEQ ID No:91)

Table 5-4

Probe No.	Base Sequence
91	g agc tcc tgg acc gcG (SEQ ID No:92)
92	g gat tac atc gcc ctg aaT (SEQ ID No:93)
93	c gac acg cag ttc gtg C (SEQ ID No:94)
94	cag atc tcc aag acc aac A (SEQ ID No:95)
95	c gga gct gtg gtc gct A (SEQ ID No:96)
96	c acc ctc cag agg atg tT (SEQ ID No:97)
97	tac gcc tac gac ggc aaA (SEQ ID No:98)
98	cag atc tgc aag acc aac A (SEQ ID No:99)
99	cg agt ccg agg atg gcT (SEQ ID No:100)
100	g ggc ctg tgc gtg gaC (SEQ ID No:101)
101	gg gcc ggc tcc cac tT (SEQ ID No:102)
102	ac atg aag gcc tcc gcG (SEQ ID No:103)
103	gca gct gtg gtg gtg cT (SEQ ID No:104)
104	gtg acc cac cac ccc G (SEQ ID No:105)
105	g tat tgg gac cgg gag aT (SEQ ID No:106)
106	gcg agt ccg agg atg gC (SEQ ID No:107)
107	c acc ctc cag agg atg tC (SEQ ID No:108)
108	gg acc gcc gcg gac aA (SEQ ID No:109)
109	g atg tac ggc tgc gac C (SEQ ID No:110)
110	g tct cac acc ctc cag aC (SEQ ID No:111)
111	ct cac acc ctc cag acG (SEQ ID No:112)
112	ac cga gag aac ctg cgC (SEQ ID No:113)
113	c ggg aag gag acg ctg C (SEQ ID No:114)
114	cc ctg aac gag gac ctg A (SEQ ID No:115)
115	g gag ccc cgc ttc atc G (SEQ ID No:116)
116	agg tat ttc tac acc gcc A (SEQ ID No:117)
117	t ccg agg atg gcg ccC (SEQ ID No:118)
118	g ttc gac agc gac gcc A (SEQ ID No:119)
119	gag ccg cgg gcg ccA (SEQ ID No:120)
120	g gcg gag cag ctg aga A (SEQ ID No:121)

Table 5-5

Probe No.	Base Sequence
121	a acc tac ctg gag ggc C (SEQ ID No:122)
122	acc tac ctg gag ggc cT (SEQ ID No:123)
123	c tcc aag acc aac aca cG (SEQ ID No:124)
124	c tac gtg gac gac acg cT (SEQ ID No:125)
125	c cgg gag aca cag atc tT (SEQ ID No:126)
126	ac aca cag act tac cga gT (SEQ ID No:127)
127	ca cag act tac cga gtg aA (SEQ ID No:128)
128	c cgc ggg cat aac cag tT (SEQ ID No:129)
129	cc cag ttc gtg agg ttc A (SEQ ID No:130)
130	c cgg gag aca cag atc tG (SEQ ID No:131)
131	g gct cag atc acc cag cA (SEQ ID No:132)
132	acc tac ctg gag ggc aC (SEQ ID No:133)
133	cac tcc atg agg tat ttc C (SEQ ID No:134)
134	gac ccc cca aag aca caT (SEQ ID No:135)
135	gag aca cag atc tcc aag aT (SEQ ID No:136)
136	gg gag gcg gcc cgt C (SEQ ID No:137)
137	gcg ccg tgg ata gag caA (SEQ ID No:138)
138	g acc aac aca cag act tac A (SEQ ID No:139)
139	ac acc ctc cag aat atg taT (SEQ ID No:140)
140	g gag ccc cgc ttc att G (SEQ ID No:141)
141	g gat tac atc gcc ctg aaG (SEQ ID No:142)
142	c acc ctc cag agg atg tG (SEQ ID No:143)
143	gcg ccg tgg ata gag caA (SEQ ID No:144)
144	cga gag aac ctg cgc aC (SEQ ID No:145)
145	gag aac ctg cgc acc gC (SEQ ID No:146)
146	g tct cac acc ctc cag aaT (SEQ ID No:147)
147	cag gag ggg ccg gag C (SEQ ID No:148)
148	ctg ggc ttc tac cct gG (SEQ ID No:149)
149	ca cag act gac cga gag G (SEQ ID No:150)
150	c gcc gcg gac acg gcA (SEQ ID No:151)

Table 5-6

Probe No.	Base Sequence
151	ctg ctc tgg ggg gca G (SEQ ID No :152)
152	c cag agc gag gcc ggT (SEQ ID No :153)
153	c tcc gtg tcc cgg ccT (SEQ ID No :154)
154	cgc ggg tac cac cag C (SEQ ID No :155)
155	tg acc gag acc tgg gcT (SEQ ID No :156)
156	cag gag ggg ccg gag tT (SEQ ID No :157)
157	cga gag agc ctg cgg aC (SEQ ID No :158)
158	c acg gcg gct cag atc T (SEQ ID No :159)
159	cg gag cag ctg aga gcT (SEQ ID No :160)
160	gg ccc gac ggg cgc T (SEQ ID No :161)
161	cgc ggg cat gac cag tT (SEQ ID No :162)
162	cc atg tcc cgg ccc gT (SEQ ID No :163)
163	g acc gcg gcg gac acC (SEQ ID No :164)
164	c tgc gac gtg ggg ccC (SEQ ID No :165)
165	t ccg agg acg gag ccC (SEQ ID No :166)
166	gag ccc cgg gcg ccA (SEQ ID No :167)
167	cc gcg agt ccg agg aC (SEQ ID No :168)
168	cac atc atc cag agg atg tT (SEQ ID No :169)
169	ca cag act tac cga gag aA (SEQ ID No :170)
170	c atg tac ggc tgc gac C (SEQ ID No :171)
171	ctg cgg aac ctg cgc gA (SEQ ID No :172)
172	cat gac cag tcc gcc tG (SEQ ID No :173)
173	c acc atc cag agg atg tC (SEQ ID No :174)
174	gac ctg agc tcc tgg acA (SEQ ID No :175)
175	cga gag agc ctg cgc aC (SEQ ID No :176)
176	g cag gag ggg ccg gG (SEQ ID No :177)
177	ga acc tac ctg gag ggc A (SEQ ID No :178)
178	a acc tac ctg gag ggc aT (SEQ ID No :179)
179	c tgg acc gcg gcg gaG (SEQ ID No :180)
180	ta gag cag gag ggg ccA (SEQ ID No :181)

Table 5-7

Probe No.	Base Sequence
181	tct cac act tgg cag acG (SEQ ID No :182)
182	g gcg gag cag cgg aga A (SEQ ID No :183)
183	cgg ccc ggc cgc ggA (SEQ ID No :184)
184	gg tct cac acc ctc caC (SEQ ID No :185)
185	c cgc ggg tat aac cag ttA (SEQ ID No :186)
186	g gcg gag cag tgg aga A (SEQ ID No :187)
187	gaa tat tgg gac cgg gaG (SEQ ID No :188)
188	gcg gct cag atc acc cG (SEQ ID No :189)
189	cac acc ctc cag agc aC (SEQ ID No :190)
190	ag tgg gag gcg gcc cT (SEQ ID No :191)
191	g acc gag acc tgg gcG (SEQ ID No :192)
192	c gcc acg agt ccg agg A (SEQ ID No :193)
193	g atc tcc cag cgc aag tT (SEQ ID No :194)
194	tg gag gcg gcc cgt gT (SEQ ID No :195)
195	tg acc gag acc tgg gcT (SEQ ID No :196)
196	g cgc tcc tgg acc gcG (SEQ ID No :197)
197	ag ggc gag tgc gtg gaT (SEQ ID No :198)
198	gg tat ttc cac acc gcc A (SEQ ID No :199)
199	c cgc ggg cat aac cag A (SEQ ID No :200)
200	ccg gag tat tgg gac cC (SEQ ID No :201)
201	gg tct cac atc atc cag G (SEQ ID No :202)
202	c gcc tac gac ggc aag A (SEQ ID No :203)
203	cgc ggg cat aac cag tC (SEQ ID No :204)
204	cc ggg tct cac act tgG (SEQ ID No :205)
205	c act tgg cag agg atg taT (SEQ ID No :206)
206	ga gag agc ctg cgg aaG (SEQ ID No :207)
207	c ggg aag gac acg ctg C (SEQ ID No :208)
208	c acg ctg cag cgc gcG (SEQ ID No :209)
209	cc atc tct gac cat gag gT (SEQ ID No :210)
210	cgg gag aca cag atc tcG (SEQ ID No :211)

Table 5-8

Probe No.	Base Sequence
211	g gag gcg gcc cgt gtC (SEQ ID No :212)
212	a gag aac ctg cgc acc G (SEQ ID No :213)
213	gg gag ccc cgc ttc atT (SEQ ID No :214)
214	ctg cgc acc ccg ctc C (SEQ ID No :215)
215	gg ccg gag tat tgg gaG (SEQ ID No :216)
216	c cgc ggg cat aac cag G (SEQ ID No :217)
217	ggc gag tgc gtg gag tC (SEQ ID No :218)
218	ccg gcg ccg tgg gtG (SEQ ID No :219)
219	ga gag aac ctg cgg atc G (SEQ ID No :220)
220	gtg gac gac acg ctg ttG (SEQ ID No :221)
221	tg gag ggc ctg tgc gC (SEQ ID No :222)
222	gac ggc aag gat tac atc A (SEQ ID No :223)
223	c cgc ggg tat aac cag tT (SEQ ID No :224)
224	ctc cgc ggg tat aac cG (SEQ ID No :225)
225	gcg gag cag gac aga gT (SEQ ID No :226)
226	gag aca cag aag tac aag C (SEQ ID No :227)
227	cgc cag gca cag act gG (SEQ ID No :228)
228	t gtg gtc gct gct gtg G (SEQ ID No :229)
229	c ctg cgg aac ctg ctc C (SEQ ID No :230)
230	aga acc ttc cag aag tgg A (SEQ ID No :231)
231	ag ccc cgc ttc atc tcC (SEQ ID No :232)
232	c cgc ggg tat aac cag ttA (SEQ ID No :233)
233	ggc ctg tgc gtg gag G (SEQ ID No :234)
234	cgg atc gcg ctc cgc G (SEQ ID No :235)
235	ttc gcc tac gac ggc aaA (SEQ ID No :236)
236	ctc ctc cgc ggg cat aaA (SEQ ID No :237)
237	g cgt ctc ctc cgc ggT (SEQ ID No :238)
238	c ggg cgc ctc ctc cC (SEQ ID No :239)
239	g agt ccg agg acg gag A (SEQ ID No :240)
240	ata gag cag gag ggg cG (SEQ ID No :241)

Table 5-9

Probe No.	Base Sequence
241	cc aga cca gca gga gat G (SEQ ID No :242)
242	cag cat gag ggg ctg cT (SEQ ID No :243)
243	cag act tac cga gag aac T (SEQ ID No :244)
244	gc gac gcc gcg agt cA (SEQ ID No :245)
245	c cgc ggg gag ccc cC (SEQ ID No :246)
246	cga gag agc ctg cgg aT (SEQ ID No :247)
247	gag agc ctg cgg atc gC (SEQ ID No :248)
248	g gca cag act gac cga gT (SEQ ID No :249)
249	g acc gcc gcg gac acC (SEQ ID No :250)
250	g cag gag ggg ccg gC (SEQ ID No :251)
251	cc gcg agt ccg aga gG (SEQ ID No :252)
252	gg tct cac act tgg cag aT (SEQ ID No :253)
253	acg gca ccc cga acc C (SEQ ID No :254)
254	ctc ctc ctg ctg ctc tG (SEQ ID No :255)
255	ag aca cag aag tac aag gG (SEQ ID No :256)
256	gg tct cac atc atc cag gT (SEQ ID No :257)
257	gc ggg cat gac cag tcT (SEQ ID No :258)
258	g acc gcg gcg gac acA (SEQ ID No :259)
259	g ccg gag tat tgg gac G (SEQ ID No :260)
260	c ctc ctc cgc ggg tat A (SEQ ID No :261)
261	c acg gcg gct cag atc aT (SEQ ID No :262)
262	tg cgg atc gcg ctc cC (SEQ ID No :263)
263	g ccg gag tat tgg gac gA (SEQ ID No :264)
264	g gag gcg gcc cgt gC (SEQ ID No :265)
265	c gac gcc gcg agt ccA (SEQ ID No :266)
266	gtc acc gta gct gtg gtC (SEQ ID No :267)
267	g tgt agg agg aag agt tcT (SEQ ID No :268)
268	c aga gcc tac ctg gag gA (SEQ ID No :269)
269	gtc atc gga gct gtg gtT (SEQ ID No :270)

Table 6-1

Probe No.	Base Sequence
0	c acc tcc Gtg tcc cgg (SEQ ID No:271)
1	c ctc cag agC atg tac gg (SEQ ID No:272)
2	c cgc ggg Cat gac cag (SEQ ID No:273)
3	cat gac cag Tac gcc tac (SEQ ID No:274)
4	g gag cag cGg aga gcc (SEQ ID No:275)
5	gag cag cGg aga gcc ta (SEQ ID No:276)
6	g gag ggc gAg tgc gtg (SEQ ID No:277)
7	c gtg gag tGg ctc cgc (SEQ ID No:278)
8	ac aag ctg GAg cgc gct (SEQ ID No:279)
9	ctc cgc agG tac ctg ga (SEQ ID No:280)
10	g gac gac acG cag ttc gt (SEQ ID No:281)
11	aag acc aac Aca cag act g (SEQ ID No:282)
12	g gag cag gaC aga gcc ta (SEQ ID No:283)
13	cgc ggg cat Aac cag tac (SEQ ID No:284)
14	cag tcc acc ATc ccc atc (SEQ ID No:285)
15	c ctc cag agG atg tac gg (SEQ ID No:286)
16	aca cag atc tTc aag acc aa (SEQ ID No:287)
17	t gac cag tCc gcc tac g (SEQ ID No:288)
18	ca cag atc tGc aag gcc c (SEQ ID No:289)
19	c cga gag aAc ctg cgg a (SEQ ID No:290)
20	tct cac atc ATc cag agg a (SEQ ID No:291)
21	g agg atg taT ggc tgc ga (SEQ ID No:292)
22	c tgc gac Ctg ggg ccc (SEQ ID No:293)
23	ctg ggg ccC gac ggg (SEQ ID No:294)
24	g tac aag cGc cag gca c (SEQ ID No:295)
25	ag gca cag Gct gac cga (SEQ ID No:296)
26	t gac cga gTg agc ctg c (SEQ ID No:297)
27	gg tct cac aTc atc cag ag (SEQ ID No:298)
28	c atc cag agG atg tac gg (SEQ ID No:299)
29	tc cgc ggg Tat gac cag (SEQ ID No:300)
30	aag acc aac Aca cag act ta (SEQ ID No:301)